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•	(7M)
	(TM)
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Sep 17 16:49:37 1998; MasPar time 10.98 Seconds 425.709 Million cell updates/sec

Tabular output not generated.

>US-08-741-437-1 (1-289) from US08741437.pep

Description: .
Perfect Score: Sequence: 2134 1 MSGFSTEERAAPFSLEYRVF.....CESACTVPTDVDKWFHHQKN 289

Scoring table: PAM 150 Gap 11

131922 seqs, 16180660 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

i:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28

Statistics: Mean 33.562; Variance 136.718; scale 0.245

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

16 8		15 8	14 8	. 13 8	12 8	11 8	10 9	9	8	7 9	6	5	4.	w	2 100	. 1 18	Result No. Score
7 4.1		88 4.1	37 4.1	87 4.1	8 4.1	9 4.2	0 4.2	0 4.2	4.3	4.3	1 4.3	1 4.3	5 4.5	7 4.5	0 4.7	15 8.7	Query e Match Length
535 13	535 5	366 3	362 2	337 2	138 17	1085 28	1079 28	274 1	715 10	713 11	366 3	354 8	350 8	345 1	716 10	176 19	ength DB
R69731	R28411	R12466	P70155	P70590	R92524	W38272	W38275	P80911	R55198	R60101	R12465	R42424	R42426	P83149	R55200	R98153	Ħ
Cyclic-GMP stimulated	Protein encoded by cD	HLA-C exon Cb-2.	Sequence encoded by g	Sequence of the human	Pyrodictium occultum	Bovine parathyroid ce	Rat kidney cell calci	Consensus sequence of	Canine zona pellucida	Canine zona pellucida	HLA-C exon Cb-1.	Rat gustducin alpha s	Bovine rod transducin	Probe F10,-encoded pro	Feline zona pellucida	Thermostable inorgani	Description
5.28e+01	5.28e+01	4.47e+01	5.28e+01	5.28e+01	4.47e+01	3.78e+01	3.19e+01	3.19e+01	2.69e+01	2.69e+01	2.69e+01	2.69e+01	1.35e+01	9.55e+00	5.63e+00	3.58e-07	Pred. No.

Query Match 8.7%; Best Local Similarity 36.9%; Matches 31; Conservative

Score 185; DB 19; Length 176; Pred. No. 3.58e-07; 20; Mismatches -30; Indels

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Gaps

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1738 4 R20192 ADH complex 1738 4 R20192 ADH complex 1738 3 R13993 A.altocetige 914 17 R92222 Pyrodictium 11078 28 W38274 Human parathyroid 11078 20 W11889 Parathyroid 11088 14 R705398 Fungus-infec 11219 24 W25763 Amino acid 21 R194 17 R34712 Bacillus sub 172 15 R86405 Alternativel 1219 24 W24986 Monoclonal a 124 W24986 Monoclonal a 134 24 W24986 HLA-B35 anti	4.4	4 4	" t	-	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	Ly
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R20192 ADH complex protet R20192 ADH complex protet R13993 A.altocetigenes n R92522 Pyrodictium occul will 88 Parathyroid calci W11888 Parathyroid calci R70633 Fungus-infected (R72398 ADH complex bedilus subtilus R86405 Alternatively spl R84049 Sequence of the V W01526 Monoclonal antibor R12464 HLA-Bw53 exon. R64159 Human elastase in R415456 Alpha-1,6-glucan R60532 Fungus-infected (R70340 Bovine diarrhoea R03142 Porcine zona pellu R73699 Novel type II R785194																		1088							38	000
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	type II	Sorcine Tona mellucid	diarrnoea	infected (	Glucan Lyase 1.	zona pellucid	-1,6-glucan-6-g	elastase inhib	elastase inhib	HLA-Bw53 exon.	đ	antibody	ntibody	the VH	splic	lis sr	sequenc	Glucan Lyase 1.	Fungus-infected G.lem		Ē	Human parathyroid cel		enes		Hippocampus carcium/c

## ALIGNMENTS

88888 8	888	88888	PT	מק קק קק אק	N S S S D D	RESULT ID R AC R
eliminate problems of pyrophosphorylosis in reactions conducted at temp. above 37 deg C; esp. when an accumulation of pyrophosphates could be a problem, e.g. thermal cycling processes utilising DNA polymerases.  Sequence 176 AA;	(T30073) into an expression vector allows prodn. of recombinant PPase in transformed host cells. The PPase may be used to	The thermostable inorganic pyrophosphatase (PPase) (R98153) of Thermococcus litoralis has a subunit mol.wt. of 20-21 kDa. It is active after 4 hr incubation at 100 deg C and retains 100% of its activity at 72 deg C. Incorporation of the isolated Ppase generativity at 72 deg C.	N-PSDB: 730073.  N-PSDB: 730073.  N-PSDB: 730073.  Thermostable inorganic pyro:phosphatase isolated from Thermococcus Intoralis - catalyses the hydrolysis of inorganic pyro:phosphate Claim 1: Page 57: 85pp: English.	02-MAY-1996. 23-OCT-1995; U13662. 25-OCT-1994; US-329721. (NEWE ) NEW ENGLAND BIOLABS INC. (LENDOX T, SCATS LE, Slatko BE;	O6-JAN-1997 (first entry) Thermostable inorganic pyrophosphatase. Inorganic pyrophosphatase; pyrophosphate phosphohydrolase; PPase; thermostable enzyme. Thermococcus litoralis strain NS-C (DSM 5473). W09612798-A1	JLT 1 R98153 standard; Protein; 176 AA. R98153;

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Best Local :
           WO8809386-A.
01-DEC-1988.
27-MAY-1987; FR-007577.
29-MAY-1987; DE LA VAILEE BS.
AUffray C. Behar G, Billa
WPI; 88-353959/49.
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A cDNA library was prepared in lambda gt10 from mRNA isolated from ovaries of 3-4 month old cats. Plaques were screened using a mixture of probes encoding porcine ZPA, ZPB and ZPC proteins.

Positive clones were analysed further by Southern hybridisation using the porcine probes and clones encoding feline ZPA, ZPB and ZPC proteins were identified. The deduced amino acid sequence (R55200) from the feline ZPA clone was approximately 75% homologous Sequence
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: US-973341.
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larity 30.2%;
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5.63e+00;
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Disclosure; Page 34; 50pp; English.

The sequence is that of bovine rod transducin. The sequence was compared to that of bovine cone transducin and a rat novel taste cell specific guanine nucleotide binding protein, gustducin, alpha subunit. Fragments of the protein possessing at least one ligand/antiligand binding activity or immunological property specific to antiligand binding activity or immunological property specifi
Rat gustducin alpha subunit.
Taste modifying agent; ligand;
taste receptor cells; sweet; bi
Rattus rattus.
W09321337-A.
                                                                                                                                  R42424;
24-MAY-1994
                                                                                                                                                                                  R42424 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qustducin are taste modifying agents taste receptor cells to modify taste, bitter, salty or sour tastes. See also R42405-36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New gustducin alpha subunit protein - used modifying agents which mimic or inhibit swe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-APR-1993; U03279.
09-APR-1992; US-868353.
(MARG/) MARGOLSKEE R F.
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Taste modifying agent; ligand; antiligand;
taste receptor cells; sweet; bitter; sweet.
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Restriction fragment length polymorphism genotyping test for chickens, using erythrocyte DNA fragments and hybridisation probe derived from histocompatibility complex antigen.
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WPI; 93-351746
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20; Conse
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llarity 30.8%;
Conservative
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8; M
                                                d; antiligand; binding
bitter; sweet; salty;
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sweet; salty; sour; gustducin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 8; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          logical property specific to which can be delivered to e.g. mimic or inhibit sweet,
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9.55e+00;
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                                                                      activity;
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Best Local S
Matches 2
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Matches
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                                                                                                                                                                                                        HIA-C gene, DNA probe and transformant cells - for immunisation of animals and monoclonal antibody development.

Claim 3; Page 2; 13pp; Japanese.

Probes comprising part of the DNA sequence encoding the protein can be used to identify Class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HIA-C antigen. See also R12466 (same patent) and J03112486
15-MAR-1995 (first entry)
Canine zona pellucida CZP2
Canine; dog; zona pellucid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of a rat novel taste cell specific quanine nucleotide binding protein, gustducin, alpha subunit. Fragments of the protein possessing at least one ligand/antiligand binding activity or immunological property specific to gustducin are taste modifying agents which can be delivered to taste receptor cells to modify taste, e.g. mimic or inhibit sweet, bitter, salty or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Margolskee RF;
WPI; 93-351746
                                                                                                                                                                                                   for the HLA-C antigen. and J03112487.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                   R60101 standard;
R60101;
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Sequence 354 AA;
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09-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                               MHC; class I.
                                                                                                                                                                                                                                                                                                                                                                                                          Human leukocyte antigen; probe;
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R12465;
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                                                                                         DAANYNDINDVKRLK-PGYLEATVDWFR-RYKVPDGKPENEFAFNAEFKDKDFAIDIIKS 222
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                                                                                                                                       h 4.3%;
Similarity 50.0%;
11; Conservative
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US-868353.
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 ZP; CZP2; contraceptive; vaccine;
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                                                                                                                                                               Length 366;
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salty or
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Best Local Similarity 30.2%;
Matches 16; Conservative
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P80911;
18-SEP-1990
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The CZP2 DNA (070072) was prepd. by the cloning of CZP2(75-520) - The CZP2 DNA (070072) was prepd. by the CZP2(1-65) - Q81804 using the primers given in Q70073-74, CZP2(1-65) - Q81804 using the primers given in Q70082-83, CZP2(42-103) - Q81957 using the primers given in Q70079-81 and CZP2(487-713) - Q81957 using the primers given in Q70079-81 and CZP2(487-713)
                                                                                                                                                                                                                                                                                                                                                        used as probes in Southern hybridisations. Sequences coding for canine ZPA and ZPC proteins were obtained (Q65608 and Q65609, respectively). R55198 is the deduced amino acid sequence for Sequence 715 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of zona pellucida proteins and antibodies - for inducing reproducible transient infertility or permanent sterility in
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A commercially available 16 week old canine ovarian cDNA expression library in lambda gtll was screened using antibodies raised agains heat solubilised canine zona pellucida. The largest candidate clor was used to rescreen the library and to isolate clones which were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; Q65608
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09-NOV-1992; US-973341.
29-JAN-1993; US-012990.
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06-NOV-1993;
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(laim 40; Page 88-90; 154pp; English.
(commercially available 16 week old canine ovarian cDNA expression
(commercially available 16 week old canine ovarian cDNA expression
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                                                                                                                                                                                  frmtvkc-hysrddllintnvqslpppvasvrpgplalilqtypdksylrpyg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pellucida ZPA protein.
Zona pellucida; ZPA; immunocontraception.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in Q70075-78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Podolski JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           canine_ZPA
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Pred. No.
12; Misma
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                                                                                                                                                                                                                                        DB 10; L... 2.69e+01; -hes 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11.
2.69e+01;
                                                                                                                                                                                                                                                                                                Length 715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 713;
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Best Local :
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23-MUG-1991; US-749451.
11-FEB-1992; US-934161.
21-AUG-1992; US-934161.
12-FEB-1993; US-017127.
23-FEB-1993; US-017127.
23-FEB-1993; US-141248.
19-AUG-1994; US-282827.
21-CCT-1994; WS-282827.
21-CCT-1994; WS-355784.
(BGHM) BRIGHAM & WOMENS H.
The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. The proteins of the number of
                                                                                                                                            receptor 3A (RakCaR 3A)
                                                                                                                                                                 DNA encoding calcium receptor polypeptide(s) therapeutic purposes, e.g. hyperparathyroidism Claim 20; Columns 133-142; 174pp; English. The present sequence is rat kidney cell calcium
                                                                                                                                                                                                                                                                                                                                                                               Brown
                                                                                                                                                                                                                                                                                                                                                                                                              (BGHM )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat kidney cell calcium receptor 3A; RakCar 3A). Rat kidney cell calcium receptor 3A; RakCar 3A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transplants or auto-immune diseases

Example 9; Fig 4; 60pp; English.

The concensus sequence is derived from a total of 23 HLA-A,B,C sequences. The protein sequences in the three extrecellular domains (alpha-1).

alpha-2 and alpha-3) are shown. The example concerned the effect of peptides from different HLA-A2 epitopes on cytolysis of target cells by CTL of different specificities.
                                                                                                                                                                                                                                                                                                                 N-PSDB; T95860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             calcium
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US5688938-A
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30-JAN-1987; US-008846.
(STRD) Leland Stanford.
Krensky AM, Parham P, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 qlra-ylegtcvewlrry-lengk 176 :|:: |||:| |:|:|| : :||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 88-235147/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of different specificities.
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egions of
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larity 50.08;
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                                 Pyrodictium occultum DNA polyn DNA pol; base pair; thermally polymerase chain reaction; di pyrodictium occultum DSM2709.
                                                                                                                                                                                                                                                                                                                                                                                                                        proteins, nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor activities, preferably disorders of calcium homeostasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding calcium receptor polypeptide(s) - therapeutic purposes, e.g. hyperparathyroidism claim 4; Columns 107-116; 174pp; English.
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19-AUG-1994;
21-OCT-1994;
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-) NPS PHARM INC.
EM, Fuller FH, Garrett JE, Hebert
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parathyroid cell calcium receptor 1; BoPCaR 1;
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19; Conser
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                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                        Protein;
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                                                                                             polymerase
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Pred.
16;- M
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                                                                     gene PCR product
e; exonuclease act
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3.78e+01;
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                                                                   activity;
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ostasis, e.
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Location/Qualifiers

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Best Local Similarity 24.18;

Matches 13; Conservative
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Best Local Similarity 21.68;
                                                                                                                                                                                                                                                                                                    Disclosure; Page 5; 5pp; German.

Disclosure; Page 5; 5pp; German.

The DNA may be used as a hybridisation probe for detecting the HLA B27 gene, eg for assessing susceptibility to rheumatic disorders such as ankylosis spondylitis, or may be used to transform cells for prodn. of HLA B27. The HLA B27 may be used to detect HLA B27 antibody in human serum, or to produce mono- or polyclonal HLA B27.
                         03-APR-1991 (first entry)
Sequence encoded by genomic DNA encoding human histocompatibility
antigen HLA-B 27.
                                                                                        T 14
P70155 standard;
P70155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        occultum and produce thermostable DNA polymerase. Also disclosed are DNA polymerase genes which hybridise to the above genes. Sequence 138 AA;
                                                           10-MAR-1993
03-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR performed on Pyrodictium occultum chromosomal DNA. Two full lenguenes encoding a 914 amino acid and an 803 amino acid DNA polymerase were later identified. The genes are derived from Pyrodictium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J07327684-A.
19-DEC-1995.
09-JUN-1994; 150591.
09-JUN-1994; JP-150591
                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     such DNA, antigen or antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA coding for antigen HLA B27 - and diagnostic reagents contg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BEHW ) BEHRINGWERKE AG.
Riethmuller G, Meo T, Weiss E, Szots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rheumatic disorder; genetic ankylosing spondylitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-APR-1991
Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 13; 23pp; Japanese
R92524 and R92525 are proteins enco
            Ankylosing spondylitis; rheumatic disorder; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; N70935.
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21-DEC-1985; DE-545576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P70590 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TAKI ) TAKARA SHUZO CO LTD
NPI; 96-072342/08.
                                                                                                                                                                       147
                                                                                                                                                                                               125 lnedlsswtaadtaagitqr-kweaarvaeqlra-ylegecvewlrry-lengk 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  )4-JUN-1987
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                                                                                                                                                                IDEGETDWKVIAINVDDPDAANYNDINDVKRLKPGYLEAT-VDWFRRYKVPDGK 199
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                                                                                                                                                                                                                                                                                         n human serum, or to pro
for use in immunoassay.
337 AA;
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                                                                           (revised)
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                                                                                                        protein;
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                                                                                                          362
                                                                                                                                                                                                                            Score 87; DB 2;
Pred. No. 5.28e+01
15; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 88; DB 17;
Pred. No. 4.47e+01
15; Mismatches 2
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                                                                                                                                                                                                                                                          Length 337;
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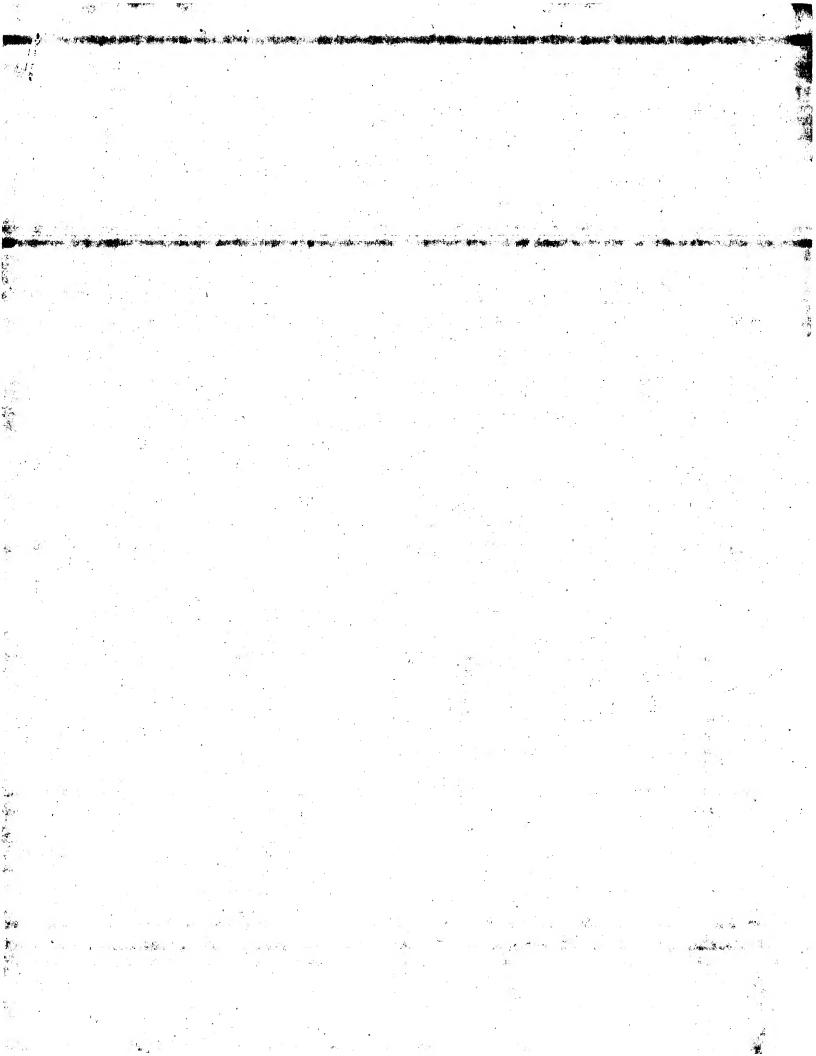
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Best Local
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R12466 standard;
R12466;
                                                                                                                         be used to identify Class I genes. The DNA can be expressed immunisation of animals and prodn. of monoclonal antibodies s for the HIA-C antigen. See also R12465 (same patent) and J03112487.
                                                                                                                                                                              of animals and monoclonal antibody development.
Claim 4; Page 2; 13pp; Japanese.
Probes comprising part of the DNA sequence encoding the protein
                                                                                                                                                                                                                            HLA-C gene, DNA probe and transformant cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; p6; 13pp; German.
THE DNA may be used to detect the HLA-B 27 gene (opt. mutated human genetic material. The HLA-B 27 may be used to detect at B 27 antibodies in human serum. The antibodies may be used to determine HLA-B 27 levels in human serum, eg for diagnosis of rheumatic disorders, esp. ankylosing spondylitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Szots H, Weiss E, Dorner C, WPI; 87-171469/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1985;
21-DEC-1985;
                                                                                                                                                                                                                                                        (OLYU ) OLYMPUS OPTICAL WPI; 91-182989/25.
                                                                                                                                                                                                                                                                                                                                                                       Human leukocyte
                                                                                                                                                                                                                                                                                                                                                                                    HLA-C exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA coding for human histocompatibility antigen for diagnosis and antigen and antibody prodn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP-226069-A
                                                                                                                                                                                                                                            N-PSDB; Q12117
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181 GYLEAT-VDWFRRYKVPDGK
                        182 aylegtovewlrry-lengk
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22-SEP-1989;
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les . 11; Conse
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13; Conser
                                                                                                            366 AA;
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larity 55.08;
Conservative
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DE-542024.
DE-545576.
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JP-247695.
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J03112486
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated Thu Sep 17 16:57:21 1998; MasPar time 3.93 Seconds 518.696 Million cell updates/sec

Run on:

>US-08-741-437-1 (1-289) from US08741437.pep

Description:
Perfect Score:
Sequence: 1 MSGFSTEERAAPFSLEYRVF......CESACTVPTDVDKWFHHQKN 289

Scoring table: PAM 150 Gap 11

Searched: 77021 seqs, 7058996 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

a-issued 1:5\_COMB 2:PCT9\_COMB 3:backfiles1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 31.457; Variance 133.821; scale 0.235

# SUMMARIES

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1.23e-07 1.23e-07 1.91e-04 1.91e-04 9.80e-02 1.45e-00 5.83e-00 9.73e-00 9.73e-00 9.73e-00 9.73e-00 9.73e-00 9.73e-00 9.73e-00 9.73e-00 9.73e-00 9.73e-00 9.73e-00 9.73e-00	Pred. No. 2.04e-89
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24 92 4.3 182 1 US-08-127 Sequence 137, Applicat 1.36e+01 25 90 4.2 182 1 US-08-127 Sequence 158, Applicat 1.36e+01 27 90 4.2 182 1 US-08-127 Sequence 158, Applicat 1.36e+01 28 90 4.2 182 1 US-08-127 Sequence 158, Applicat 1.36e+01 28 90 4.2 182 1 US-08-127 Sequence 164, Applicat 1.36e+01 29 4.2 182 1 US-08-127 Sequence 153, Applicat 1.36e+01 29 4.2 182 1 US-08-127 Sequence 145, Applicat 1.36e+01 29 4.2 274 1 US-08-127 Sequence 1, Applicati 1.36e+01 29 4.2 374 1 US-08-121 Sequence 1, Applicati 1.36e+01 29 4.2 375 2 PCT-US93-0 Sequence 8, Applicatio 1.36e+01 29 4.2 1079 1 US-08-484 Sequence 8, Applicatio 1.36e+01 29 4.2 1079 1 US-08-485 Sequence 8, Applicatio 1.36e+01 29 4.2 1085 1 US-08-485 Sequence 5, Applicatio 1.36e+01 29 4.2 1085 1 US-08-485 Sequence 5, Applicatio 1.36e+01 29 4.2 1085 1 US-08-485 Sequence 5, Applicatio 1.36e+01 29 4.2 1085 1 US-08-127 Sequence 5, Applicatio 1.36e+01 29 4.2 1085 1 US-08-127 Sequence 138, Applicatio 1.36e+01 29 4.2 1085 1 US-08-127 Sequence 139, Applicatio 1.51e+01 29 4.2 108 2 US-08-127 Sequence 139, Applicatio 1.51e+01 29 4.2 108 2 US-08-127 Sequence 139, Applicatio 1.51e+01 29 4.2 108 2 US-08-127 Sequence 139, Applicatio 1.51e+01 29 4.2 108 2 US-08-127 Sequence 139, Applicatio 1.51e+01 29 4.2 108 2 US-08-127 Sequence 139, Applicatio 1.51e+01 29 4.2 108 2 US-08-127 Sequence 170, Applicatio 1.91e+01 29 4.2 108 2 US-08-454 Sequence 49, Applicatio 2.25e+01 25 25 25 25 25 25 25 25 25 25 25 25 25			٠.																					
4.3 182 1 US-08-127- Sequence 137, Applicat US-08-127- Sequence 166, Applicat US-08-127- Sequence 158, Applicat US-08-127- Sequence 158, Applicat US-08-127- Sequence 164, Applicat US-08-127- Sequence 164, Applicat US-08-127- Sequence 164, Applicat US-08-127- Sequence 153, Applicat US-08-127- Sequence 1, Application US-08-127- Sequence 1, Application US-08-22- Sequence 1, Application US-08-121- Sequence 8, Application US-08-121- Sequence 8, Application US-08-121- Sequence 8, Application US-08-484- Sequence 8, Application US-08-484- Sequence 8, Application US-08-485- Sequence 5, Application US-08-127- Sequence 5, Application US-08-127- Sequence 139, Application US-08-127		45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	
4.3 182 1 US-08-127 Sequence 137, Applicat 4.2 182 1 US-08-127 Sequence 166, Applicat 4.2 182 1 US-08-127 Sequence 158, Applicat 4.2 182 1 US-08-127 Sequence 135, Applicat 4.2 182 1 US-08-127 Sequence 145, Applicat 4.2 182 1 US-08-127 Sequence 145, Applicat 4.2 182 1 US-08-127 Sequence 145, Applicat 6.2 182 1 US-08-222 Sequence 145, Applicat 6.2 182 1 US-08-127 Sequence 1, Applicatio 6.2 185 1 US-08-127 Sequence 8, Applicatio 6.2 187 1 US-08-121 Sequence 8, Applicatio 6.2 187 1 US-08-121 Sequence 8, Applicatio 6.2 187 1 US-08-484 Sequence 8, Applicatio 6.2 187 1 US-08-485 Sequence 8, Applicatio 6.2 187 1 US-08-485 Sequence 5, Applicatio 6.2 188 1 US-08-127 Sequence 138, Applicatio 6.2 182 1 US-08-127 Sequence 131, Applicat 7.2 182 1 US-08-127 Sequence 170, Applicat 7.2 182 1 US-08-128 Sequence 170, Applicat 7.2 182 1 US-08-128 Sequence 6, Applicatio 7.2 182 1 US-08-128 Sequence 170, Applicat 7.2 182 1 US-08-128 Sequence 6, Applicatio 7.2 182 1 US-08-128 Sequence 6, Applicatio 7.2 182 1 US-08-128 Sequence 6, Applicatio 7.2 182 1 US-08-128 Seq		.87	87	88	88	æ	œ	88	89	89	90	90	90	90	90	90	89	89	90	90	90	90	92	
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US-08-127- Sequence 137, Applicat US-08-127- Sequence 166, Applicat US-08-127- Sequence 158, Applicat US-08-127- Sequence 135, Applicat US-08-127- Sequence 145, Applicat US-08-127- Sequence 145, Applicat US-08-127- Sequence 145, Applicati US-08-127- Sequence 1, Applicatio US-08-121- Sequence 8, Applicatio US-08-121- Sequence 8, Applicatio US-08-121- Sequence 8, Applicatio US-08-185- Sequence 8, Applicatio US-08-484- Sequence 5, Applicatio US-08-485- Sequence 5, Applicatio US-08-485- Sequence 138, Applicatio US-08-127- Sequence 111, Applicat US-08-127- Sequence 113, Applicat US-08-127- Sequence 170, Applicat US-08-125- Sequence 6, Applicatio US-08-484- Sequence 6, Applicatio US-08-484- Sequence 6, Applicatio US-08-485- Sequence 170, Applicati		1088	535	182	182	182	182	182	1085	1085	1079	1079	375	375	354	274	182	182	182	182	182	182	182	
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7, Applicat 6, Applicat 18, Applicat 18, Applicat 4, Applicat 3, Applicat 3, Applicat 6, Applicat 6, Applicat 6, Applicat 6, Applicat 6, Applicati 6, Applicati 6, Applicati 7, Applicat 1, Applicat 1		Sequence (				Œ			Sequence :							(D								
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LENGTH: 286 amino acids	DICTION.	INFORMATION FOR SEO ID NO. 3.	TELEFAX: (508) 927-1705	TELEPHONE: (508) 927-5054	TELECOMMUNICATION INFORMATION:	REFERENCE/DOCKET NUMBER: NEB-105-PCT	101	NAME: WILLIAMS, GREGORY D.	۲	FILING DATE: 25-OCT-1994	TI FOR MC	ADDITON NITHERED ITC 08 /330 731	PRIOR APPLICATION DATA:	CLASSIFICATION:	FILING DATE:	APPLICATION NUMBER: PCT/US95/13662A			ເກ	'COMPUTER: IBM PC compatible	MEDIUM TYPE: Floppy disk	COMPUTER READABLE FORM:	ZIP: 01915		3	ш	STREET: 32 TOZER ROAD	ADDRESSEE: NEW ENGLAND BIOLABS, INC.	CORRESPONDENCE ADDRESS:	NUMBER OF SEQUENCES: 28	LITORALIS	TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS		SEARS, Lauren 1	SLATKO, Barton	APPLICANT: LENNOX, Tricia L.	GENERAL INFORMATION:	Sequence 3, Application PC/TUS9513662A		Sequence 3, Application PC/TUS9513662A				xxxxx		LT 1 PCT-US95-13662A-3 STANDARD: PRT: 286 AA	

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TOPOLOGY: unknown
MOLECULE TYPE:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application PC/TUS9513662A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KEETLNPIIODTKKGKLRFVRNCFPHHGYIHNYGAFPQTWEDPNVSHPETKAVGDNDPID 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 YTTRQIGAKNTLEYKVYIEKD-GKPVSAFHDIPLYADKENNIFNMVVEIPRWTNAKLEIT 60
                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LENNOX, Tricia L. APPLICANT: SLATKO, Barton E. APPLICANT: SEARS, Lauren E.
                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS
   TELECOMMUNICATION INFORMATION
                                                         FILING DATE: 25-OCT-1994 ATTORNEY/AGENT INFORMATION:
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               REGISTRATION NUMBER: 30 REFERENCE/DOCKET NUMBER
                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
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l Similarity 53.0%;
l51; Conservative
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                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                   APPLICATION NUMBER: PCT/US95/13662A
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                                                                                                                                                                                                                                                                                                    BEVERLY
                                            WILLIAMS,
                                                                                                                                                                                                                                                                                     MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                 32 TOZER ROAD
                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                           IBM PC compatible
                                                                                                                                                                                                                                                                                                                                NEW ENGLAND BIOLABS,
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                                         GREGORY D
                                                                                                                                                                                                                                                                                                                                                                             LITORALIS
                                                                                                                                                                                                                                                                                                                                                                                          PURIFIED THERMOSTABLE INORGANIC
PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
                                                                                      US 08/329,721
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Pred. No. 2.04e-89;
60; Mismatches 64
                           30901
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                 NEB-105-PCT
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Best Local :
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Local Similarity 36.9%;
                                          TELEPHONE: (508) 927-5:
TELEFAX: (508) 927-170
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
INFORMATION FOR SEQ ID NO: 10
                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 25-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D
                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                          REGISTRATION NUMBER:
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176 AA; 20659 MW; 160121 CN;
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             amino acid
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unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tricia L.
Barton E.
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Pred. No. 2.28e-07
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               Query Match
Best Local (
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SEQUENCE 179 AA; 20465 MW; 177070 CN;
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                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 7.7%;
Local Similarity 30.5%;
les 32; Conservative
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                                                                                                                                                     TELEFAX: (508) 927-1705
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                      TOPOLOGY: unknown MOLECULE TYPE: prote 164 AA; 18792
                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 25-OCT-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                             TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                                                            REGISTRATION NUMBER: 3090: REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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               Similarity
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                                                                                                                                                                                                                                       WILLIAMS, GREGORY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MASSACHUSETTS
                                                                                                                       164 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLATKO, Barton E.
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                                                                                                                                                                                  (508)
                                                        protein
18792 MW;
               7.2%;
33.3%;
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                                                                                                unknown
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                                                                                                                                                                                 927-5054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LITORALIS
                                                        MW; 129342 CN
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Score 154; DB 2; Le
Pred. No. 1.07e-04;
18; Mismatches 35;
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Pred. No. 1.23e-05;
31; Mismatches 38
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                                            113 EDLPQHKLKEIAHFFERYKDLQGK 136
 162
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                                                                                                          Match 7.18;
Local Similarity 37.18;
                                                                                                                                                                                                                                                                      TELEFAX: (508) 927-17
                                                                                                                                                        MOLECULE TYPE: protein 
JENCE, 263 AA; 29712 MW; 339305 CN;
                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (508),927-5054
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: '25-OCT-199-
ATTORNEY/AGENT INFORMATION
NAME: WILLIAMS, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LENNOX, Tricia L. APPLICANT: SLATKO, Barton E. APPLICANT: SEARS, Lauren E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
EL 163
                             CGDNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDIN 173
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                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 309
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US (FILING DATE: 25-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                           Conservative
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                                                                                                          Score 151; DB 2;
Pred. No. 1.91e-04;
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                                          US-08-127-954-165
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                                                                                                                                                                                         65 DGDPVDV-LVPTPYPLQPGSVIRCRPVGVLKMTDEAGEDAKLVAVPHSKL-SKEYDHIKD 122
                                                                                                                                                                                                                             Match 5.5%;
Local Similarity 32.2%;
les 28; Conservative
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (508) 927-1705
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS;
LENGTH: 175 amino acids
                                                                                                                                                                                                                                                                                         TOPOLOGY: un MOLECULE TYPE: DUENCE 175 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION
TELEPHONE: (508) 927-5054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/
FILING DATE: 25-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                   VKRLKPGYLEATVD-WFRRYK-VPDGK 199
                                                                                                                                                            DNDPIDVCEIGSKVCAR-GEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDIND 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                        unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEW ENGLAND BIOLABS, INC
                                                                                                                                                                                                                                                                                       protein
19572 MW; 155266 CN;
                                                                                                                                                                                                                                                                                                                                     unknown
                                        STANDARD;
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                                                                                                                                                                                                                          Score 118; DB 2;
Pred. No. 9.80e-02;
20; Mismatches 33
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                                     PRT;
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                                     182 AA.
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                                                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                       Length 175;
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                                                                                                                                                                                                                                                                                                                              147 IDEGETDWKVIAINVDDPDAANYNDINDVKRLKPGYLEAT-VDWFRRYKVPDGK 199
                                                                                                                                                                                                                                                                                                                                                            126 LNEDLRSWTAADMAAQITQR-KWETAHEAEQLRA-YLEGTCVEWLRRY-LENGK 176
                                                                                                                          Sequence 146, Application US/08127954 Patent No. 5451512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 165, Application US/08127954
                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (510) 814-297
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
UENCE 182 AA; 21175 MW; 151183 CN;
                              TITLE OF INVENTION:
                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,954
CORRESPONDENCE ADDRESS:
                                                                              APPLICANT:
                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 88
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 07110-1199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                 4.8%;
ilarity 25.9%;
Conservative
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                                                                         Bugawan;
                                                                                        Apple, Raymond J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bugawan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apple, Raymond J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (510)
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) Kingsland Street
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               Locus DNA Typing
173
                                        Methods and Reagents for HLA Class I A
                                                                           Teodorica L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Locus DNA Typing
173
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                                                                                                                                                                                                                                                                                                                                                                                                Score 103; DB 1;
Pred. No. 1.45e+00;
17; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165:
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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/07868353A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 LNEDLRSWTAADMAAQITKR-KWEAAHEAEQLRA-YLDGTCVEWLRRY-LENGK 176
                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application
                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (510) 814-2977 INFORMATION FOR SEQ ID NO: 146:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 4.78;
Local Similarity 24.18;
                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com
              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19920409
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TELECOMMUNICATION INFORMATION:
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NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                     APPLICANT: Margolskee, Robert
TITLE OF INVENTION: Gustducin
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ٥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 07110-1199
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CLASSIFICATION:
                                                                                                                                                                   COUNTRY:
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182 AA; 21058 MW; 149365 CN;
                                                                                                                                                                                 Chicago
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                                                                                                                                                                                                                                                                       Marshall,
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                                                                                                                                                                                                                                                                                                                       Ree, Robert F.
Gustducin Materials and Methods
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                                US/07/868,353A
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Pred. No. 2.06e+00;
17; Mismatches 20
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RESULT
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Best Local
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US-07-868-353A-15
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/07868353A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 THDHW 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 ERKKW 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 DAANYNDINDVKRL-KPGYLEATVDWFR-RYKVPDGKPENEFAFNAEFKDKDFAIDIIKS 222
                                                                                                                                                                                                                                                                                                                                                          Patent No. 5688662
GENERAL INFORMATION:
APPLICANT: Margol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 4.5%;
Local Similarity 30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: AMINO ACID
        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 350 AA; 39965 MW; 627049 CN;
                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 346-5750
                                                                                                         ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Margolskee, TITLE OF INVENTION: Gus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                               TELEFAX: (312) 984-9740
TELEX: 25-3856
                                                                                                                                                                                                                                                                       STREET: Two Fir
                                                                                                                                 APPLICATION NUMBER: FILING DATE: 19920
                                                                                                                                                                                                                                                  CITY: Chicago
STATE: Illinois
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                                                   TELEPHONE:
                                                                         REFERENCE/DOCKET NUMBER:
                                                                                     REGISTRATION NUMBER:
                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                            ZIP: 60603
                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshal
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                                                                            FICATION:

/AGENT INFORMATION:

NO. 5688662and, Greta E.

NO. 9700 NIMBER: P-35,302
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25-3856
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Gustducin Materials and Methods
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                                                                                                                                                                   Release #1.0, Version
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P-35,302
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Pred. No. 5.1
17; Mismatc
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5.83e+00;
                                                                                                                                                                                                                                                                                     20 South Clark
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Query Match
Best Local Similarity
Conserv

Conservative

4.5%;

Score 97; DB 1; I Pred. No. 4.14e+00; 15; Mismatches 24

24;

Gaps

Length 354

SEQUENCE

MOLECULE TYPE: protein
FEATURE: protein: /note= "Positions indicated as Xaa
OTHER INFORMATION: represent nonconserved amino acids."

974 AA: 40403 MW; 673372 CN;

20 **д**.

150 DSAXYY-LNDLDRLTAPGYVPNEQDVLRSRVKTT-GIIETQFSFK-DLNFRMFDVGGQRS 206

165 DAANYNDINDVKRLK-PGYLEATVDWFR-RYKVPDGKPENEFAFNAEFKDKDFAIDIIKS 222

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TOPOLOGY:

TYPE: AMINO ACID

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RESULT -11
ID US-08-127-954-142
Best Local Similarity
               Query Match
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                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                TOPOLOGY: 1ii
MOLECULE TYPE:
UENCE 182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bugawan, Teodórica L.
APPLICANT: Erilich, Henry A.
TITLE OF INVENTION: Methods and Reagents
TITLE OF INVENTION: Locus DNA Typing
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 88
RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 07110-1199
                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                             STRATION NUMBER: 35,321
                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Jersey
                                                                                                                              182 amino acids
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                                                                                                                                                                                (510)
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                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0,
                                                                                   linear
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27.78;
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                                                  (genomic)
2 MW; 160101 CN
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                                                                                                                                                                                                                                                                                                                                US/08/127,954
 Score 92; DB 1; Length 182; Pred. No. 9.73e+00;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
JENCE 182 AA; 21163 MW; 148760 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
. NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
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CORRESDONT
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07110-1199
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larity 25.9%;
Conservative
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Erlich, Henry
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Pred. No. 9.73e+00;
15; Mismatches 21
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Matches 14; Conser
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ENCE 182 AA; 21125 MW; 1500
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NAME: PETTY, DOUGLAS A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 88
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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                         CORRESPONDENCE ADDRESS:
                                              TITLE OF INVENTION:
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PPLICANT: Erlich, Henry A.

ITLE OF INVENTION: Methods and Reagents for HLA Class I A

ITLE OF INVENTION: Locus DNA Typing
                                                                                     PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: New Jo
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larity 25.9%;
Conservative
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  E: Hoffmann-La Roche Inc
340 Kingsland Street
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Erlich, Henry
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Locus DNA Typing
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173
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Pred. No. 9.73e+00;
15; Mismatches 21
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Best Local Similarity 25.9%;
Matches 14; Conservative
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                           COMPUTER READABLE FORM:
MEDIDIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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JENCE. 182 AA; 21022 MW; 147718 CN;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
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LENGTH: 182 amino acids
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NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,
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APPLICANT: Apple, Raymond J.
APPLICANT: Bugawan, Teodoric
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
APPLICATION NUMBER: US/00 FILING DATE: CLASSIFICATION: 436 ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION:
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CITY: Nutley
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Erlich, Henry A.
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                                  US/08/127,95
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Pred. No. 9.73e+00;
15; Mismatches 21
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Length 182;

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Gaps

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CC REFERENCE/DOCKET NUMBER: 35,321
CC REFERENCE/DOCKET NUMBER: 3873
CC REFERENCE/DOCKET NUMBER: 3873
CC REFERENCE/DOCKET NUMBER: 3873
CC REFERENCE/DOCKET NUMBER: 3873
CC TELECOMMUNICATION INFORMATION:
CC TELECOMMUNICATION INFORMATION:
CC TELEPAX: (510) 814-2974
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CC TELEPAX: (510) 814-2974
CC TELEPAX: (510) 814-2974
CC TYPE: anino acids:
CC TYPE: anino acids:
CC TYPE: DNA (genomic)
CC TOPOLOGY: linear
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC SEQUENCE 182 AA; 21161 MW; 161123 CN;
CQ SEQUENCE 182 AA; 21161 MW; 161123 CN;
CQ SEQUENCE 182 AA; 27.7%; Pred: No. 9.73e+00;
CO SEQUENCE 182 AA; 27.7%; Pred: No. 9.73e+00;
CO SEQUENCE 182 AA; 21.61 MISMATCHES 17; Indels 4; Gaps 4;
CO MATCHES 13; CONSERVATIVE 13; MISMATCHES 17; Indels 4; Gaps 4;
CO MATCHES 13; WISMATCHES 17; Indels 11; III; III; III; III; III;
CO SEQUENCE 182 AA; 21.61 MISMATCHES 17; Indels 4; Gaps 4;
CC TOPOLOGY: 1.10 MISMATCHES 17; Indels 4; Gaps 4;
CC TOPOLOGY: 1.10 MISMATCHES 17; Indels 4; Gaps 4;
CC TOPOLOGY: 1.10 MISMATCHES 17; Indels 4; Gaps 4;
CC TOPOLOGY: 1.10 MISMATCHES 17; Indels 4; Gaps 4;
CC TOPOLOGY: 1.10 MISMATCHES 17; Indels 4; Gaps 4;
CC TOPOLOGY: 1.10 MISMATCHES 17; Indels 4; Gaps 4;
CC TOPOLOGY: 1.10 MISMATCHES 17; Indels 4; Gaps 4;
CC TOPOLOGY: 1.10 MW; 161123 CN;
CC TOPOLOGY: 1.10 MW; 1
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COMMENT
KEYWORDS
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54-159,137-143
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8,56,58,78,89,93,
15,117,120,147,
52,154,192,193
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                                                                                                                                       267, 2-9, 16-21,
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Asp,
#length 282
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The structural basis for pyrophosphatase catalysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heikinheimo, P.; submitted to the
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New crystal forms of e. coli and
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Asp, Lys, Tyr, Lys #label ASB
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152,154,192,193
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93 #site Glu, Lys, Glu, Arg, Tyr, Tyr, Asp,
Asp, Lys, Tyr, Lys #label ASA
#length 283 #molecular-weight 31941 #checksı
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New crystal forms of e. coli and
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The structural basis for pyropho
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on: 2.2 angstroms
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Local Similarity 53.0%;
nes 151; Conservative
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Structure of inorganic pyrophosphatase from e. coli and its
complex with a mn2+ ion at 2.2 angstroms resolution.
                                                                       Kankare, J.; Neal, G.S.; Salminen, T.; Glumhoff, Cooperman, B.S.; Lahti, R.; Goldman, A. Protein Eng. (1944) 7:823
The structure of e. coli soluble inorganic pyropl
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New crystal forms of escherichia coli and saccharomyces cerevisiae soluble inorganic pyrophosphatases.
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X-ray structure of yeast inorganic pyrophosphatase complexed
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   Baykov, A.A.; Shestakov, A.S.
Eur. J. Biochem. (1992) 206:463
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Protein Sci. (1994) 3:1098
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S.S.; Popov, A.N.; Rubinskiy, S.V.; Vainshtei
zarova, T.I.; Kurilova, S.A.; Vorobyova, N.N.;
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Determination: X-ray diffraction
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Eur. J. Biochem. (1974) 47:57
Yeast inorganic pyrophosphatase:
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Kristallografiya (1990) 35:1581
The growing of crystals of inorganic pyrophosphatase
The growing of crystals of inorganic pyrophosphatase
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The mechanism of action
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Bioorg. Khim. (1984) 10:1469
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H.; Samejima, T.; Kuranova, I.
Protein Sci. (1994) 3:1098
Crystal structure of inorganic pyrophosphatase
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                                                                                          Acta Crystallogr. (1995) D51:399
New crystal forms of escherichia coli and saccharomyces
cerevisiae soluble inorganic pyrophosphatases.
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V.S.; Dauter, Z.;
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Pred. No. 5.83e-166;
58; Mismatches 68;
                                                                                                                                                                                                                                                                                      T.I.; Kurilova, S.A.;
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A.V.; Wilson,
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Eur. J. Biochem (1974) 47:57
Yeast inorganic pyrophosphatase:
Resolution: 2.4 angstroms
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Cooperman, B.S.; Lahti, R.; Goldman,
Protein Eng. (1994) 7:823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. (1984) 259:2886
Investigations of the metal ion-binding
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Eur. J. Biochem. (1992) 206:463
Two pathways of pyrophosphate hydrolysis
yeast inorganic pyrophosphatase.
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The mechanism of action of yeast
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The growing of crystals of inorganic pyrophosphatase yeast with metal ions and phosphate (Russian).
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Crystal structure of mnpi comp
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Bioorg. Khim. (1986) 12:749
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X-Ray diffraction study of inorganic pyrophosphatase from
baker's yeast at the 3 angstroms resolution (Russian).
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Smirnova,
                                                                       x-ray structural investigation of inorganic pyrophosphatase of baker yeast. I. Growing of crystals, production of derivatives and determination of the heavy atom positions
                                                                                                                                                                                                                                                                                             Makhaldianei, V.V.; Smirnova, E.A.; Voronova, A.A.; Tovbis, A.B.; Kuranova, I.P.; Arutyunyan, E.G.; Vainshtein, B.K.; Bienwald, B.; Hansen, G.; Hoehne, W.E. Sov. Phys. Crystallogr! (1980) 25:163
X-ray structural investigation of inorganic pyrophosphatase of yeasts. II. calculation of phases and structural model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kristallografiya (1980) 25:280
X-ray structural investigation of inorganic pyrophosphatase
of baker yeast. II. phase calculation and structure model
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Covalent structural analysis of yeast inorganic
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                                                                                                                                                                                                                                                                                                                                                                                                              Determination: X-ray diffraction R-value: 0.172
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Resolution:
                                                   134; Conservative
                                                                   h 45.7%;
Similarity 57.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ppase structure of inorganic pyrophosphatase
                                                                                                                    #33 #site Glu, Lys, Glu, Arg, Tyr, Tyr, Asp, Lys, Tyr, Lys #label ASB #length 234 #checksum 1513
                                                                                                                                                                                                                                                                                                                                                                                           hydrolase; manganese; pyrophosphate phosphohydrolase
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New crystal forms of e. coli and
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inorganic pyrophosphatase (EC 3.6.1.1) metal complex,
B, fragment 1 - yeast (Saccharomyces cerevisiae)
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                                                 Score 976; DB 5; I
Pred. No. 2.68e-155;
48; Mismatches 49.
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                                                                                                                                                                                                                                        LKPGYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWKALVTKKTNG
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Similarity 48.6%;
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(Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #active_site Arg #status predicted
#length 289 #molecular-weight 32467 #checksum 5076
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Nucleotide sequence of S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawasaki, I.;
                                                                               A40867 #type complete
inorganic pyrophosphatase (EC 3.6.1.1)
mitochondrial - yeast (Saccharomyces
protein YM8156.09; protein YMR267w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       formal_name Schizosaccharomyces
                                                    #formal_name Saccharomyces cerevisiae
27_Mar-1992 #sequence_revision 27-Mar-1992 #text_change
                         A40867; S54479
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M.; Baltscheffsky,
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                                                                ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #cross-references EMBL:Z49260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                                                                                  YFPGILDTTREWFRKYKVPAGKPLNSFAFHEQYQNSNKTIQTIKKCHNSWKNLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSTIQQGSKYTLGFKKYLTLLNGEVGSFFHDVPLDLNEHEKTVNMIVEVPRWTTGKFEIS
                                                                                                                                                                                                                                                                                                                                                                                LKPGYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWKALVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPLDCCEIGSDVLEMGSIKKVKVLGSLALIDDGELDWKVIVIDVNDPLSSKIDDLEKIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TKDPLNPIKQDVKKGKLRYVANLFPYKGYIWNYGAIPQTWEDPGHNDKHTGC-C---GDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KELRFNPIVQDTKNGKLRFVNNIFPYHGYIHNYGAIPQTWEDPTIEHKLGKCDVALKGDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSTEERAAPFSLEYRVFLKNEKGQYISPFHDIPI-YADKD-VFHMVVEVPRWSNAKMEIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lye, G.; Church submitted to 1 S54479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. (1991) 266:12168-12172
Yeast PPA2 gene encodes a mitochondri
pyrophosphatase that is essential f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S5401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #superfamily inorganic pyrophosphatase
hydrolase; mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGD:PPA2; IPP2
                                                                                                  Richter, O.M.H.; Schaefer, G.
Eur. J. Blochem. (1992) 209:351-355
Cloning and sequencing of the gene fc
inorganic pyrophosphatase from the
archaebacterium Thermoplasma acidop
                                                                                                                                                                                                                       #formal_name Thermoplasma acidophilum
22-Jan-1994 #sequence_revision 10-Nov
09-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #length 310
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                                                                                      S29313
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                                                                                                                                                                                                                                                                                          inorganic
#length 179
                   hydrolase
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function.
                                                                                                                                                                                                                                                                            acidophilum
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#label MAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-310 ##label LYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #domain transit peptide (mitochondrion) #status
                                                    1-179 ##label RIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.1%;
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                                                                                                                                                                                                                                                                                        pyrophosphatase
                                                                                                                                                                                                                                                                                                              #type complete
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   #molecular-weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 812; DB 2; I
Pred. No. 2.99e-124;
51; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , C.M.
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NID: g172222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NID: 9809081;
                                  NID: 948081; PID: 948082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Library, May
                                                                                                                                                                                                                                                                                              (EC 3.6.1.1)
                                                                                                    gene for the cytoplasmic
om the thermoacidophilic
acidophilum.
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                                                                                                                                                                                                                                             10-Nov-1995
   20465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 310
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   #checksum
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                                                                                                                                                                                                                                                                                               Thermoplasma
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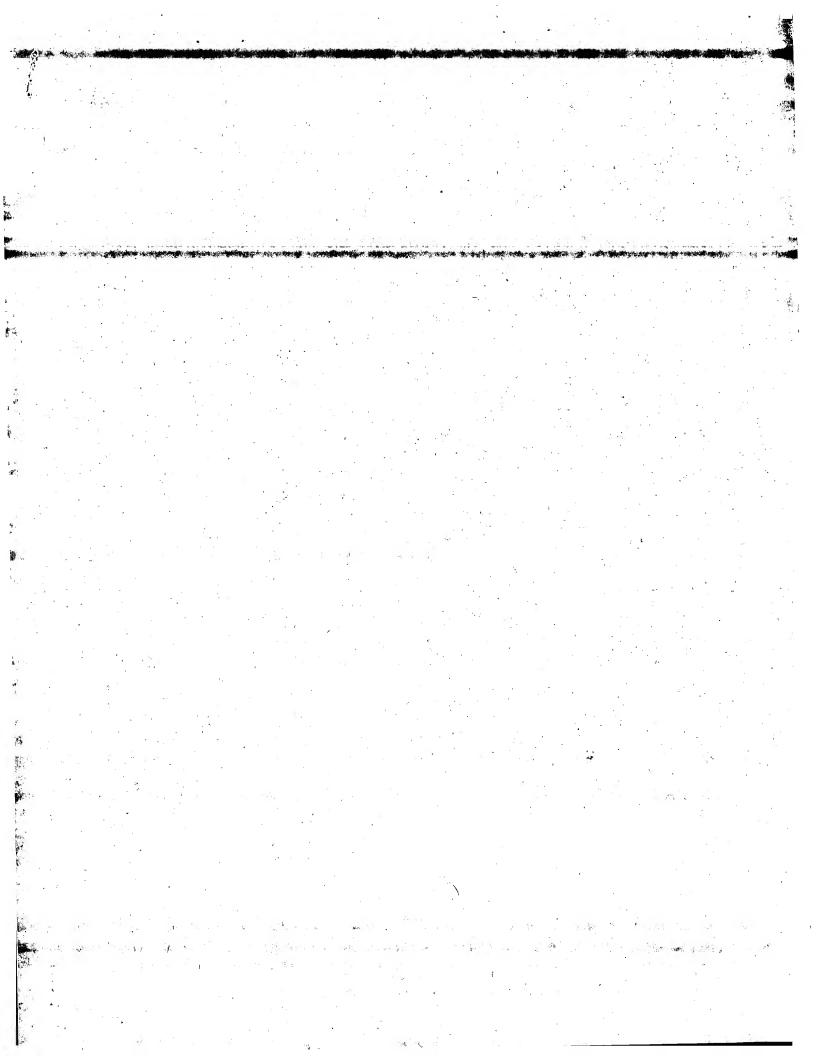
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KEYWORDS
FEATURE
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ENTRY
TITLE
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12,22
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                                                                         COMMENT
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best
                                                                                                                        #authors Ichiba, T.; Takenaka, O.; Samejima, T.; Hachimori, A.
#journal J. Biochem. (1990) 108:572-578
#title Primary structure of the inorganic pyrophosphatase from
thermophilic bacterium PS-3.
#cross-references MUID:91154162
#accession JX0135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type protein
##residues 1-164 ##label SAT
##experimental_source strain ATCC 12016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 KRLKPGYLEATVDWFRRYKVPDGKPENEFAFNA-EFKDKDFAIDI 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type protein
##residues 1-164 ##label ICH
This enzyme is a trimer of identical chains. It catalyzes the
hydrolysis of pyrophosphate to orthophosphate in the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 KRLKPGYLEATVDWFRRYKVPDGK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 EDLPQHKLKEIAHFFERYKDLQGK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 KDVNAHLLDEIANFFSTYKILEKKETKVLGWEGKEAALKEIEVSI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 DNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.2%;
Local Similarity 33.3%;
nes 28; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 7.7%;
Local Similarity 30.5%;
hes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 DGDPMDVMVLISQPTFPGAIMKVRPIGMMKMVDQGETDNKILAVFDKDPNVS-Y--IKDL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primary structure, overexpression, characterization and crystallization of inorganic pyrophosphatase from Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Satoh, T.; Ishii, K.; Koyama, M.; Sakurai, N.; Kaji, H.; Hachimori, A.; Irie, M.; Samejima, T. submitted to JIPID, April 1997
                                                                                                                                                                                                                                                                                               pyrophosphate phosphohydrolase
#formal_name thermophilic bacterium PS-3
30-Jun-1992 #sequence_revision 30-Jun-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #formal_name Bacillus stearothermophilus
28-May-1997 #sequence_revision 18-Jul-1997 #text_change
18-Jul-1997
                                                                                                                                                                                                                                                                                                                                                           inorganic pyrophosphatase (EC 3.6.1.1) - thermophilic
bacterium PS-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #active_site Glu #status predicted
#length 164 #molecular-weight 18796 #checksum 5644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hydrolase
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                     hydrolase
                                                                                                                                                                                                                                                                                 28-Apr-1993
                                                                                                                                                                                                                                                                                                                                                                                              #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 165; DB 2; Pred. No. 3.42e-09; 31; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 154; DB 2;
Pred. No. 1.37e-07;
18; Mismatches 35
                                                                                                                                                                                                                                                                                                 30-Jun-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
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74-156
SUMMARY
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                                                                                                           Query Match
Best Local
                                                                                          Matches
113 EDLPQHKLKEIAHFFERYKDLQGK 136
                              116
                                                         56 DGDPLDILVITTNPPFPGCVIDTRVIGYLNMVDSGEEDAKLIGVPVEDP---RFDEVRSI 112
                            DNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDV 175
                                                                                                      7.2%;
Similarity 33.3%;
                                                                                          28;
                                                                                                                                                    #disulfide_bonds #status experimental
#length 164 #molecular-weight 18792 #checksum
                                                                                          Conservative
                                                                                          18;
                                                                                                        Score 154; DB 2;
Pred. No. 1.37e-07;
                                                                                          Mismatches 35;
                                                                                                                       Length 164;
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Search completed: Thu Sep 17 16:53:28 1998 Job time: 68 secs.

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176 KRIKPGYLEATVDWFRRYKVPDGK 199



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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Sep 17 16:53:45 1998; MasPar time 10.59 Seconds 684.218 Million cell updates/sec

Tabular output not generated

Description: Perfect Score: Sequence: Title:

>US-08-741-437-1 (1-289) from US08741437.pep 2134 1 MSGFSTEERAAPFSLEYRVF......CESACTVPTDVDKWFHHQKN 289

Scoring table: PAM 150 Gap 11

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 47.360; Variance 80.422; scale 0.589

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	% Query Match	Length	DB	Ħ	Description	Pred. No.
1	2063	96.7	289	ㅁ¦	IPYR_BOVIN	INORGANIC PYROPHOSPHAT	0.00e+00
ν.	1035	48.5	286	Н	IPYR_YEAST		1.47e-213
ω	1019	47.8	286	۲	IPYR_KLULA		1.19e-209
4	939	44.0	288	Н	IPYR_SCHPO	INORGANIC PYROPHOSPHAT	3.83e-190
5	812	38.1	310	بر	IPY2_YEAST	G	2.35e-159
6	658	30.8	114	Ь	IPYR_HUMAN	INORGANIC PYROPHOSPHAT	2.02e-122
7	185	8.7	176	ص	IPYR_THELI	THERMOSTABLE INORGANIC	3.54e-16
8	165	7.7	179	щ	IPYR_THEAC	INORGANIC PYROPHOSPHAT	2.21e-12
٩	154	7.2	164	Н	IPYR_BACP3	INORGANIC PYROPHOSPHAT	2.31e-10
10	151	7.1	263	44	IPYR_ARATH	SOLUBLE INORGANIC PYRO	8.03e-10
11	. 149	7.0	173	سا	IPYR_SULAC	INORGANIC PYROPHOSPHAT	1.83e-09
12	147	6.9	177	H	IPYR_BARBA	INORGANIC PYROPHOSPHAT	4.16e-09
13	147	6.9	211	۳.	IPYR_SOLTU	SOLUBLE INORGANIC PYRO	4.16e-09
14	125	5.9	184	<u>,</u>	IPYR_MYCPN	INORGANIC PYROPHOSPHAT	2.43e-05
15	122	5.7	176	۲	IPYR_HAEIN	PROBABLE INORGANIC PYR	7.51e-05
16	119	5.6	173	Н	IPYR_HELPY	INORGANIC PYROPHOSPHAT	2.28e-04
17	117	5.5	169	ب	IPYR_SYNY3	INORGANIC PYROPHOSPHAT	4.74e-04
18	118	5.5	175	ب	IPYR_ECOLI	INORGANIC PYROPHOSPHAT	3.29e-04
19	117	5.5	184	١_4	IPYR_MYCGE	INORGANIC PYROPHOSPHAT	4.74e-04
20	112	5.2	174	L	IPYR_THETH	INORGANIC PYROPHOSPHAT	2.86e-03
21	110	5.2	1102	_	YE20_METJA	HYPOTHETICAL PROTEIN M	5.79e-03
22	107	5.0	814	_	CADF_HUMAN	MUSCLE-CADHERIN PRECUR	1.64e-02
23	104	4.9	365	1	1A03_GORGO	CLASS I HISTOCOMPATIBI	4.56e-02
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24 103 4.8 352 1 1B36_HUMAN HLA CLASS I HISTOCOMPA 25 100 4.7 362 1 1B03_GORGO CLASS I HISTOCOMPATIBI 26 100 4.7 362 1 1B03_GORGO CLASS I HISTOCOMPATIBI 27 100 4.7 362 1 1B03_GORGO CLASS I HISTOCOMPATIBI 28 100 4.7 362 1 1B01_SAGOE CLASS I HISTOCOMPATIBI 30 100 4.7 365 1 1A01_SAGOE CLASS I HISTOCOMPATIBI 31 101 4.7 365 1 1A01_SAGOE CLASS I HISTOCOMPATIBI 31 101 4.7 376 1 1ZP2_FELCA 32 100 4.7 716 1 ZP2_FELCA 33 101 4.7 716 1 ZP2_FELCA 34 99 4.6 365 1 1A04_PANTE CHLA CLASS I HISTOCOMPA 35 101 4.7 788 1 CL14_NEUGR CHLA CLASS I HISTOCOMPA 36 99 4.6 365 1 1A04_PANTE CHLA CLASS I HISTOCOMPA 37 98 4.6 365 1 1A04_PANTE CHLA CLASS I HISTOCOMPA 38 99 4.6 365 1 1A04_PANTE CHLA CLASS I HISTOCOMPA 39 99 4.6 369 1 HALB_MOUSE H-2 CLASS I HISTOCOMPA 30 99 4.6 369 1 HALB_MOUSE H-2 CLASS I HISTOCOMPA 31 99 4.6 370 1 CADF_MOUSE H-2 CLASS I HISTOCOMPA 32 99 4.6 3430 1 POLG_WIN GENOME POLYPROTEIN (CO 4.0 97 4.5 343 1 HOLG_HUMAN HLA CLASS I HISTOCOMPA 4.7 365 1 HALB_HUMAN HLA CLASS I HISTOCOMPA 4.8 362 1 HALB_HUMAN HLA CLASS I HISTOCOMPA 4.9 36 4.5 362 1 HALB_HUMAN HLA CLASS I HIST							,						,									
4.8 362 1 1856_HUMAN HLA CLASS I HISTO 4.8 3124 1 CAHC_CHICK COLLAGES I HISTOCOMP. 4.7 362 1 1801_GORGO CLASS I HISTOCOMP. 4.7 362 1 1801_GORGO CLASS I HISTOCOMP. 4.7 365 1 1801_SAGOE CLASS I HISTOCOMP. 4.7 365 1 1801_SAGOE CLASS I HISTOCOMP. 4.7 365 1 1A01_SAGOE CLASS I HISTOCOMP. 4.7 370 1 1A03_HUMAN HLA CLASS I HISTOCOMP. 4.7 716 1 ZP2_FELCA ZONA PELLUCIDA SP. 4.7 718 1 CY14_NEUCR CHLASC I HISTOCOMP. 4.7 718 1 CY14_NEUCR CLASS I HISTOCOMP. 4.6 365 1 1A04_PANTR CHLA CLASS I HISTOCOMP. 4.6 365 1 1C18_HUMAN HLA CLASS I HISTOCOMP. 4.6 365 1 1C18_HUMAN HLA CLASS I HISTOCOMP. 4.6 3430 1 POLG_MOV GENOME POLYPROTEI 4.5 345 1 HAIF_CHICK CLASS I HISTOCOMP. 4.5 349 1 GBT1_HUMAN HLA CLASS I HISTOCOMP. 4.5 349 1 GBT1_HUMAN HLA CLASS I HISTOCOMP. 4.5 349 1 HAIF_CHICK CLASS I HISTOCOMP. 4.5 340 1 HAIF_CHICK CLASS I HISTOCOMP. 4.5 340 1 HAIF_CHICK CLASS I HISTOCOMP. 4.5 340 1 HAIF_CHICK CL	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
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1 1855_HUMAN HLA CLASS I HISTO 1 CAIC_CHICK COLLAGEN ALPHA 1[1] 1 1803_GORGO CLASS I HISTOCOMP. 1 1801_GORGO CLASS I HISTOCOMP. 1 1801_GORGO CLASS I HISTOCOMP. 1 1801_SAGOE CLASS I HISTOCOMP. 1 1801_HUMAN HLA CLASS I HISTOCOMP. 1 1812_MUSE H-2 CLASS I HISTOCOMP. 1 1812_MUSE H-2 CLASS I HISTOCOMP. 1 1812_MUSE H-2 CLASS I HISTOCOMP. 1 1812_HUMAN HLA CLASS I HISTOCOMP. 1 1812_HUMAN HLA CLASS I HISTOCOMP. 1 1819_HUMAN HLA CLASS I HISTOCOMP. 1 1848_HUMAN HLA CLASS I HISTOCOMP.	4.5	4.5	4.5	4.5	4.5	4.5	4.6	4.6	4.6	4.6	- <b>4</b> . 6	4.6	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.8	4.8
CHICK CCLASS I HISTOCOMP. GORGO CLASS I HISTOCOMP. GORGO CLASS I HISTOCOMP. GORGO CLASS I HISTOCOMP. GORGO CLASS I HISTOCOMP. SAGOE CLASS I HISTOCOMP. SAGOE CLASS I HISTOCOMP. SAGOE CLASS I HISTOCOMP. SAGOE CLASS I HISTOCOMP. LOWAN HIA CLASS I HISTOCOMP. PANTR CHLA CLASS I HISTOCOMP. HUMAN HIA CLASS I HISTOCOMP. MOUSE MUSCLE-CADHERIN P. METJA HYPOTHETICAL POTEI CHICK CLASS I HISTOCOMP. HUMAN GENOME POLYPROTEI CHICK CLASS I HISTOCOMP. HUMAN HIA CLASS I HISTOCOMP.	385	362.	362	358	349	345	3430	1750	730	369	366	365	788	716	370	365	365	362	362	362	3124	362
CHICK CCLASS I HISTOCOMP. GORGO CLASS I HISTOCOMP. SAGOE CLASS I HISTOCOMP. SAGOE CLASS I HISTOCOMP. SAGOE CLASS I HISTOCOMP. SAGOE CLASS I HISTOCOMP. CASS I HISTOCOMP. PANTR CHAR CLASS I HISTOCOMP. PAUGAN HIA CLASS I HISTOCOMP. MOUSE MUSCLE-CADHERIN P. M	بإ	_	<u>س</u> ر	بسر	ب		٠	بر	_	۲	Ļ	ب	_	_	بر	Ь	ب	ب	_	<b></b>	۳	۳
CASS I HISTO SEN ALPHA 1[ I HISTOCOMP. LASS I HISTO. E POLYPROTEI I HISTOCOMP. NE NUCLEOTID. NE NUCLEOTID. LASS I HISTO. LA	YPSC_BACSU	1B48_HUMAN	1B19_HUMAN	HLAE_HUMAN	GBT1_HUMAN	HA1F_CHICK	POLG_WNV	Y832_METJA	CADF_MOUSE	HA1B_MOUSE	1C18_HUMAN	1A04_PANTR	CY14_NEUCR	ZP2_FELCA	1A03_HUMAN	1B01_SAGOE	1A01_SAGOE	1B02_GORGO	1B01_GORGO	1B03_GORGO	CA1C_CHICK	
	43.5	CLASS I	CLASS I	CLASS I		I HISTOCOMPAT	POLYPROTEIN	HYPOTHETICAL PROTEIN M	MUSCLE-CADHERIN PRECUR	CLASS	CLASS I	CHLA CLASS I HISTOCOMP	SULFATE PERMEASE II.	ZONA PELLUCIDA SPERM-B		I HIST	H	H	н	CLASS I HISTOCOMPATIBI	COLLAGEN ALPHA 1(XII)	CLASS I

# ALIGNMENTS

망	Qy Db	Qy Db	Mae Qu	SQ	XX	R		8	88	88	e e	38	RL	<b>R</b> 3	N R	RP .	R C	88	80	GN	J 1	ij	ΔŢ	ΩŢ	AC	Ħ	RESU	
121 DVCEIGSKVCARGEIIRVKVLGILAMIDEGETDWKVIAINVEDPDAANYNDINDVKRLKP 180	61 ATKDPLNPIKQDVKKGKLRYVANLFPYKGYIWNYGAIPQTWEDPGHNDKHTGCCGDNDPI 120 	1 MSSFSSEERAAPETLEYRVFLKNEKGQYISPFHDIPIYADKEVFHMVVEVPRWSNAKMEI 60 	Query Match 96.7%; Score 2063; DB 1; Length 289; Best Local Similarity 94.8%; Pred. No. 0.00e+00; Matches 274; Conservative 11; Mismatches 4; Indels 0; Gaps 0;	ACT_SITE 57 57 BY SIMILARITY. SEQUENCE 289 AA; 32844 MW; ALD512C4 CRC32;	HYDROLASE; MAGNESIUM.	HSSP; P00817; 1PYP.	EMBL; M95283; -; NOT_ANNOTATED_CDS. PIR; A45153; A45153.	-!- SIMILARITY: TO OTHER PPASES.	SEGMENTS.	7	- I SUBCELLI A IOCATION. CYTODIASMIC	I - CATA		YANG Z., WENSEL T.G.:		SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	[1]				INORGANIC PIROPHOSPHATASE (EC 3.5.1.1) (PIROPHOSPHATE PHOSPHO:	7 (REL. 35, LAST ANNOTATION UPDATE)	(REL. 30,	01-OCT-1994 (REL. 30, CREATED)		IPYR BOVIN STANDARD: PRT: 289 AA.	ULT 1	ALIGNMENTS

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181 181

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241 241

SCMNTTVSESPFQCDPDAAKAIVDALPPPCESACTIPTDVDKWFHHQKN 289

SCMNTTLSESPFKCDPDAARAIVDALPPPCESACTVPTDVDKWFHHQKN

289

STANDARD;

PRT;

286

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121 DVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRLKP

GYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKNFAIDIIESTHDYWRALVTKKTDGKGI 240

GYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWKALVTKKTNGKGI

240

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AC
   SEQUENCE OF 239-249.
STRAIN=ATCC 38531 / Y
MEDLINE; 97089742.
NORBECK J., BLOMBERG
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KOLAKOWSKI L.F. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.
MEDLINE; 78087552
COHEN S.A., STERN
               SIMILARITY TO E.COLI AND K.LACTIS PPASES.
MEDLINE; 90254161.
LAHTI R., KOLAKOWSKI L.F. JR., HEINONEN
                                                                           HEIKINHEIMO P., LEHTONEN J.,
GOLDMAN A.;
STRUCTURE 4:1491-1508(1996).
                                                                                                                                                                                                                                                               BOND
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE: 95203288.
GARRELS J.I., FUTCHER B., KOBAYASHI R.,
VOLPE T., WARNER J.R., MCLAUGHLIN C.S.;
ELECTROPHORESIS 15:1466-1486(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBMITTED (AUG-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEIC ACIDS RES.
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 COOPERMAN
                                                                                                                                                                                  ARUTIUNIAN E.G., TERZIAN
SMIRNOVA E.A., VAINSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PP1 OR PPA1 OR PPA OR YBR011C OR
ACCHAROMYCES CEREVISIAE (BAKER'S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YDROLASE) (PPASE)
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1-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)

1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

NORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
                                                                                                                                                                                                                                             ACTIVE SITE.

SOND M.W., CHIU N.Y., COOPERMAN B.S

SIOCHEMISTRY 19:94-102(1980).
                                                                                                                                                                                                                                                                                                     ORBECK J., BLOMBERG A.;
PEMS MICROBIOL, LETT. 137:1-8(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRAIN=S288C;
                                                                                                                          EDLINE; 97148342
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                                                                                                                                       -RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE OF 25-35 AND 239-251.
                                                                                                                                                                                                                  RAY CRYSTALLOGRAPHY (3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOL.
                                                                                                                                                                      AKAD. NAUK SSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A., STERNER R., KEIM P.S.,
CHEM. 253:889-897(1978).
KOLAKOWSKI L.F. JR., B.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16:10441-10452(1988).
                                                                                                                                                                                                                                                                                                                                                       Y41;
                                                                                                                                                                       258:1481(1981).
                                                                                                                                                                                    3.0 ANGSTROMS).
N S.S., VORONOV
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T., S
                                                                                                           BAYKOV A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M., LI Z., THERMANN R.; SCHAAFF-GERSTENSCHLAEGER
                                                                                                                                                                                      YORONOVA A.A.,
HOHNE W.E., HI
                   HEINONEN J.,
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                                                                                                           LAHTI
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HANSEN G.;
                 VIHINEN
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                                                                                                              COOPERMAN
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                    POHJANOKSA K.,
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EMBL; Z35880; G53620
PIR; S45864; PWBY.
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-!- SUBCELLULAR LOCATION: CYTOPI
-!- SIMILARITY: TO OTHER PPASES
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                                    SEQUENCE
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l Similarity
151; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  )PAGE; P00817;
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                                    286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G536206;
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        48.5%;
                                    32184 MW;
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                                                                                                                                                                                                                                                                                                                                  D (IN REF. 3).
D -> N (IN REF. 3).
MISSING (IN REF. 3).
E -> Q (IN REF. 3).
Q -> E (IN REF. 3).
Q -> D (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC
Score 1035;
Pred. No. 1.
60; Mismatc
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INORGANIC |
N -> D (IN
D -> N (IN
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 Mismatches
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Matches 14
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01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE HYDROLASE) (PPASE).
                                                                                                                                                                                                                                                                                     ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 89189093.
STARK M.J.R., MILNER J.S.;
YEAST 5:35-50(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIOCHIM. BIOPHYS. ACTA 1038:338-345(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 90254161.
LAHTI R., KOLAKOWSKI L.F. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY TO E.COLI AND YEAST PPASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; FUNGI; ASCOMYCOTINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COOPERMAN B.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [PYR_KLULA
| 13998;
                 179
                                            121
                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LUYVEROMYCES LACTIS (YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                             I- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = I- COFACTOR: THIS ENZYME REQUIRES THE PRESENCE CATION. MAGNESIUM CONFERS THE HIGHEST ACTIVII- SUBUNIT: HOMODIMER.
                                                                                                    61
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                                                                                                                                                                      1 SYTTROVGAKNSLDYKVYIEKD-GKPISAFHDIPLYADEANGIFNMVVEIPRWTNAKLEI 59
                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: CYTOPLASMIC SIMILARITY: TO OTHER PPASES.
                                                      DVLEIGEQVAYTGQVKQVKVLGVMALLDEGETDWKYIAIDINDPLAPKLNDIEDVEKHL- 178
                                                                                                              S07894; PWVKL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLRATNEWFRIYKIPDGKPENQFAFSGEAKNKKYALDIIKETHDSWKQLIAGKSSDSKGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLEIGETIAYTGQVKQVKALGIMALLDEGETDWKVIAIDINDPLAPKLNDIEDVEKYFPG
PGLLRATNEWFRIYKIPDGKPENQFAFSGEAKNKKYTLDVIRECNEAWKKLISGKSADAK
                                         DVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDV-KRLK
                                                                                                 ATKDPLNPIKQDVKKGKLRYVANLFPYKGYIWNYGAIPQTWEDPGHNDKHTGCCGDNDPI
                                                                                                                                                        GFSTEERAAPFSLEYRVFLKNEKGQYISPFHDIPIYADK-D-VFHMVVEVPRWSNAKMEI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWKALVT-KKTNGKGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRLKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKDPLNPIKQDVKKGKLRYVANLFPYKGYIWNYGAIPQTWEDPGHNDKHTGCCGDNDPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEETLNPIIQDTKKGKLREVRNCFPHHGYIHNYGAFPQTWEDPNVSHPETKAVGDNDPID 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCMNTTLSESPFKCDPDAARAIVDALPPPC-ESACTVPTDVDKWF
                                                                                                                                                                                                                                                                                                                                                                                     X14230; G2903;
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                          0817; 1PYP.
PS00387; PPASE;
                                                                                                                                                                                                                                                                                                             MAGNESIUM.
                                                                                                                                                                                                                                                                      286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                            47.8%;
                                                                                                                                                                                                                                                                   56 F
78 I
32034 MW;
                                                                                                                                                                                                              Score 1019; DB 1;
Pred. No. 1.19e-209;
66; Mismatches 63;
                                                                                                                                                                                                                                                                  BY SIMILARITY.
PROBABLE.
INORGANIC PYROPHOSPHATE
748339D5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEINONEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIHINEN M.,
                                                                                                                                                                                                                                       Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF DIVALENT METAL
                                                                                                                                                                                                              Indels 10;
                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
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                                                                                                                                                                                                              Gaps
              238
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RESULT
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Best Local S
Matches 13
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[1]
SEQUENCE FROM N.A.
MEDLINE; 91016938.
MEDLINE; 91016938.
MEDLINE; 91016938.
MEDLINE; 11, ADACHI N., IKEDA H.;
PES. 18:5888-5888(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIHINUEN M., LUNDIN M., BALTSCHEFFSKY H.;
BIOCHEM. BIOPHYS. RES. COMMUN. 186:122-128(1992).
-I- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
-I- COFACTOR: THIS ENZYME REQUIRES THE PRESENCE OF DIVALENT METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-CT-1994 (REL. 30, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPYR_SCHPO P19117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i - SUBCELLULAR LOCATION: CYTOPLASMIC.
-i - SIMILARITY: TO OTHER! PPASES.
EMBL; X54301; G5014; -.
PIR; S11496; S11496.
                                                                           239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPA1 OR PPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NORGANIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SEYTTREVGALNTLDYQVYVEKN-GTPISSWHDIPLYANAEKTILNMVVEIPRWTQAKLE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATION. MAGNESIUM CONFERS THE HIGHEST SUBUNIT: HOMODIMER.
                                                                           G-ISCMNTTLSESPFKCDPDAARAIVDALPPPCESACTVPTDVDKWF
                                                                                                                              SDFSLVNVSVTGSVAN-DPSVSSTIPPA-QEL-APA-PVDPSVHKWF
                                                                                                                                                                                                            MPGLIRATNEWFRIYKIPDGKPENSFAFSGECKNRKYAEEVVRECNEAWERLITGKTDAK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GISCMNTTLSESPFKCDPDAARAIVDALPPPCESACTVPTDVDKWF
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                                                                                                                                                                               KPGYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWKALVTKKTNGK 238
                                                                                                                                                                                                                                                                               IDVCEIG-SKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRL
                                                                                                                                                                                                                                                                                                                                LDVCEIGEARGYT-GQVKQVKVLGVMALLDEGETDWKVIVIDVNDPLAPKLNDIEDVERH 178
                                                                                                                                                                                                                                                                                                                                                                                      IATKDPLNPIKQDVKKGKLRYVANLFPYKGY IWNYGAIPQTWEDPGHNDKHTGCCGDNDP
                                                                                                                                                                                                                                                                                                                                                                                                                                      ITKEATLNPIKQDTKKGKLRFVRNCFPHHGYIWNYGAFPQTYEDPNVVHPETKAKGDSDP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWKALVT-KKTNGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PPASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.08;
larity 48.48;
Conservative
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57
79
32336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 939; DB 1; I
Pred. No. 3.83e-190;
66; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INORGANIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.6.1.1) (PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEED9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYROPHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                           284
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IPY2\_YEAST: ST: P28239; 01-DEC-1992 (REL.

STANDARD:

PRT;

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24, CREATED)

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IPYR_HUMAN

IPYR_HUMAN

O15181;

O15181;

T 01-NOV-1997 (REL. 35, CREATED)

T 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

O1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

JT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE INORGANIC PYROPHOSPHATASE (EC.3.6.1.1) (PYROPHO

DE INORGANIC PYROPHOSPHATASE) (FRAGMENT):
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_S
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01-OCT-1996 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M81880; G172223; -. EMBL; Z49260; G809090; -. PIR; A40867; A40867.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIOCHEM. BIOPHYS. RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WEDLINE, 92337585.
VIHINEN M., LUNDIN M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-W303-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SACCHAROMYCES CEREVISIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PYROPHOSPHATE PHOSPHO-HYDROLASE)
IPP2 OR PPA2 OR YMR267W OR YM8156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INORGANIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYDROLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3D-STRUCTURE MODELLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYE
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                                                                                                                                                                     178
                                                                                                                                                                                              214
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                                                                                                                                                                                                                                                  154
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les 113; Consel
                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                    94
                                                                                                                                                                                                                                                                                                                                                      34 FSTIQQGSKYTLGFKKYLTLLNGEVGSFFHDVPLDLNEHEKTVNMIVEVPRWTTGKFEIS 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STIMULATED BY UNCOUPLERS OF ATP SYNTHESIS.

CATALITIC ACTIVITY: PYROPHOSPHATE + H(2)0 = 2 ORTHOPHOSPHATE.

PYROPHOSPHATASE THAT IS ESSENTIAL FOR MITOCHONDRIAL FUNCTION.

SUBUNIT: HOMODIMER THAT BINDS NONCOVALENTLY TO A PROTEIN COME
IN THE INNER MITOCHONDRIAL MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: MITOCHONDRIAL SIMILARITY: TO OTHER PPASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INEN M., LUNDIN M., BALTSCHEFFSKY H.;
CHEM. BIOPHYS. RES. COMMUN. 186:122-128(1992).
FUNCTION: INVOLVED IN ENERGY PRODUCTION. ITS
                                                                                                                                                                                                                                                                                          KELRFNPIVQDTKNGKLRFVNNIFPYHGYIHNYGAIPQTWEDPTIEHKLGKCDVALKGDN 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L0001469; PPA2
[TE; PS00387; P]
                                                                                                                                                                    LKPGYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWKALVT
                                                                                                                                                                                             YEPGILDTTREWERKYKVPAGKPLNSFAFHEQYQNSNKTIQTIKKCHNSWKNLIS
                                                                                                                                                                                                                        DPLDCCEIGSDVLEMGSIKKVKVLGSLALIDDGELDWKVIVIDVNDPLSSKIDDLEKIEE
                                                                                                                                                                                                                                                                                                                               FSTEERAAPFSLEYRVFLKNEKGQYISPFHDIPI-YADKD-VFHMVVEVPRWSNAKMEIA
                                                                                                                                                                                                                                                                            TKDPLNPIKQDVKKGKLRYVANLFPYKGYIWNYGAIPQTWEDPGHNDKHTGC-C---GDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S288C / AB972;
CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A.;
ED (MAY-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91286226
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                                                                                                                                                                                                                                                                                                                                                                                                                                   31
89
310 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BALTSCHEFFSKY H., RONNE H. 
HEM. 266:12168-12172(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNGI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRION;
                                                                                                                                                                                                                                                                                                                                                                                38.1%;
larity 48.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASCOMYCOTINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPASE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              30
310
                                                                                                                                                                                                                                                                                                                                                                                                                                   89
.35572
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LAST
                                                                                                                                                                                                                                                                                                                                                                                                                                      WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSIT PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE UPDATE)
ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MITOCHONDRIAL PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                Score 812; DB 1; I
Pred. No. 2.35e-159;
51; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MITOCHONDRION (POTENTIAL) INORGANIC PYROPHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                    C1DC143B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PPASE).
                                                     (PYROPHOSPHATE PHOSPHO-
                                                                                                                                                                                                                                                                                                                                                                                   65;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 310,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EC 3.6.1.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SI
                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEX
                                                                                                                                                                       232
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                            117
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                                                                                        Query Match
Best Local
                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA;
EUTHERIA; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
LACROIX J., VIGNERON
SUBMITTED (MAR-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
METAZOA; CHORDATA;
                                                                                                                                                                                                     LENNOX T.L., SEARS L.E., MORAN L.S., SLATKO B.E.;
SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDD DATA BANKS.
SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDD DATA BANKS.
-!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)0 = 2 PHOSPHATE.
-!- COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYDROLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                HYDROLASE; MAGNESIUM.
ACT_SITE 30 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: CYTOPLASMIC
-!- SIMILARITY: TO OTHER PPASES.
                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                          rHERMOCOCCUS LI'
ARCHAEBACTERIA;
                                                                                                                                                                                                                                                                                                                             01-NOV-1997
01-NOV-1997
                                                                                                                                                     PROSITE;
                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                         PHOSPHO-HYDROLASE)
                                                                                                                                                                                                                                                                                                                    THERMOSTABLE
                                                                                                                                                                                                                                                                                                                                                                    PYR_THELI
                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY:
  176
                   126 -P-KA-FLDEIAHFFQRYKELQGK 146
                                        116
                                                                                                                                                                                  !- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                           99
                                                                                                                                                                                             - SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                -NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HOMODIMER (BY SIMILARITY)
                                                   KRLKPGYLEATVDWFRRYKVPDGK
                                        DNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDV
                                                                                                                                                   U49440; G1518483; -. TE; PS00387; PPASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z48605; G727225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
83; Conser
                                                                              h 8.7%;
Similarity 36.9%;
31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00387; PPASE;
                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAGNESIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 AA; 13045 MW;
                                                                                                                       176 AA;
                                                                                                                                                                                                                                                                                                                            (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114
                                                                                                                                                                                                                                                                           LITORALIS.
IA; CRENARCHAEOTA;
                                                                                                                                                                                                                                                                                                                REL. 35, CREATED)
REL. 35, LAST SEQUENCE UPDATE)
REL. 35, LAST ANNOTATION UPDATE)
INORGANIC PYROPHOSPHATASE (EC 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                          Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114
                                                                                                                                                                       OTHER PPASES
                                                                                                                                                                                                                                                                                                         (PPASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.8%;
                                                                                                                       20659 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M., KEDINGER C.;
TO EMBL/GENBANK/DDBJ DATA
TY: PYROPHOSPHATE + H(2)0 =
                                                                                                                                  30
                                                                                                                                                                                   CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 658; DB 1; L
pred. No. 2.02e-122;
21; Mismatches 10;
                                                                               Score
Pred.
20; M
                                                                                                                        BY SIMILARITY.
; 3DB64F1F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERTEBRATA;
   199
                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42DF6303 CRC32;
                                                                                                                                                                                                                                                                            THERMOPROTEALES; THERMOCOCCACEAE
                                                                               e 185; DB 1; Le
. No. 3.54e-16;
Mismatches 30;
                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                      176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                     ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TETRAPODA;
                                                                                                                                                                                                                                                                                                                    3.6.1.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BANKS.
2 ORTHOPHOSPHATE
                                                                                                  Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                Indels
                                                                                                                                                                                                                                                                                                                   (PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                               114
                                                                                                                                                                                                                                                                                                                                                                                                            196
                                                                                Gaps
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                       01-FEB-1991
01-NOV-1997
INORGANIC PY
                                                                    ICHIBA T., TAKENAKA O., SAMEJIMA T., HACHIMORI A.;

J. BIOCHEM. 108:572-578 (1990).

-i- CATALYTIC ACTIVITY: SYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.

-i- COFACTOR: THIS ENZYME REQUIRES THE PRESENCE OF DIVALENT METAL

CATION. MAGNESIUM CONFERS THE HIGHEST ACTIVITY.

-i- SUBBUNIT: HOMOTRIMER. IN PRESENCE OF DIVALENT CATIONS THE TRIMI
                                                                                                                                                                                                                                              IPYR_BACP3
P19514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPYR_THEAC P37981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RICHTER O.-M.H.,
EUR. J. BIOCHEM.
                                       AGGREGATE TO FORM A HEXAMER.
-!- SUBCELLULAR LOCATION: CYTOPI
-!- SIMILARITY: TO OTHER PPASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RICHTER O.-M.H., SCHAEFER G.;
EUR. J. BIOCHEM. 209:343-349(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THERMOPLASMA ACIDOPHILUM.
ARCHAEBACTERIA; EURYARCHAEOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1994 (REL.
01-FEB-1995 (REL.
                                                                                                                                                                PROKARYOTA;
                                                                                                                                                                          BACILLUS PS3
                                                                                                                                                                                              HYDROLASE) (PPASE).
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             HYDROLASE; MAGNESIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-DSM 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYDROLASE) (PPASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INORGANIC PYROPHOSPHATASE
                                                                                                                                 EDLINE; 91154162
                                                                                                                                                                                                                                                                                                 176
                                                                                                                                                                                                                                                                                                                  124 KDVNAHLLDETANFFSTYKILEKKETKVLGWEGKEAALKEIEVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-22, MEDLINE; 93011146.
                                                                                                                                             EQUENCE.
                                                                                                                                                                                                                                                                                                                                         116
                                                                                                                                                                                                                                                                                                                                                           67 DGDPMDVMVLISQPTFPGAIMKVRPIGMMKMVDQGETDNKILAVFDKDPNVS-Y--IKDL 123
                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IR; S29313; S29313.
                                                                                                                                                                                                                                     -FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: TO OTHER PPASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC
                                                                                                                                                                                                                                                                                                KRLKPGYLEATVDWFRRYKVPDGKPENEFAFNA-EFKDKDFAIDI
                                                                                                                                                                                                                                                                                                                                       DNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              x64200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P17288; 1EIP
                      P17288;
                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93011147.
                                                                                                                                                                                                    91 (REL. 17, CREATED)
91 (REL. 17, LAST SEQUENCE UPDATE)
97 (REL. 35, LAST ANNOTATION UPDATE)
PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
                                                                                                                                                                                                                                                                                                                                                                                                                          179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REL.
                                                                                                                                                                FIRMICUTES; EN
                              JX0135.
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G48082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTIVITY: PYROPHOSPHATE + AR LOCATION: CYTOPLASMIC.
                     1EIP.
                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCHAEFER G.;
209:351-355(1992).
          PPASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                         31 I
20465 MW;
                                                                                                                                                                                                                                                                                                                                                                                            30.5%;
                                                                                                                                                                                                                                                                                                                                                                                                      7.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAST
LAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
                                                                                                                                                               IC BACTERIUM PS-3)
ENDOSPORE-FORMING
                                                 CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Og
Og
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ANNOTATION UPDATE)
(EC 3.6.1.1) (PYROP
                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                           Score 165; DB 1;
Pred. No. 2.21e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
CC7397F6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THERMOPLASMALES
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                       164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PYROPHOSPHATE PHOSPHO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H(2)0 =
                                                                                                                                                                                                                                                       A
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                                                                                                                                                               RODS
                                                                                                                                                                                                                                                                                                                                                                                38;
                                                                                                                                                                AND
                                                                                                                                                                                                                                                                                                                                                                                                   Length 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                   168
                                                                                                                                                               COCCI; BACILLACEAE
                                                                                                                                                                                                                                                                                                 219
                                                                      THE TRIMERS
                                                                                                                                                                                                                                                                                                                                                                                - 4;
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                                                                                                                                                                                                                                                                              IPYR_SUI
P50308;
                                                                                                                                                                     01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST ANOTATION
01-OCT-1996 (REL. 34, LAST ANOTATION
INORGANIC PYROPHOSPHATASE (EC 3.6.1.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X57545; G16348;
PIR; S13379; S13379
HSSP; P17288; 1EIP
PROSITE; PS00387; PPAS
SEQUENCE FROM N.A.,
STRAIN-DSM 639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 91370878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1992 (REL. 21, CREATED)
01-MAR-1992 (REL. 21, LAST SEQUENCE UP:
01-NOV-1997 (REL. 35, LAST ANNOTATION
SOLUBLE INORGANIC PYROPHOSPHATASE (EC
                                                                                                   SULFOLOBUS ACIDOCALDARIUS
                                                                                                                                                   HYDROLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYDROLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIEBER J.J., SIGNER E.R.;
PLANT MOL. BIOL. 16:345-348(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYDROLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPYR_ARATH P21216;
                                                                         ARCHAEBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAPPARALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARABIDOPSIS THALIANA (MOUSE-EAR EUKARYOTA; PLANTA; EMBRYOPHYTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 CEDSDPMDVLVLMQEPVLTGSFLRARAIGLMPMIDQGEKDDKIIAVCADDPEFRHYRDIK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116
                                                                                                                                                                                                                                                                                                                                                                                                            174 DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 EL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 CGDNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDIN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 KRLKPGYLEATVDWFRRYKVPDGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)0 = 1- COFACTOR: ACTIVITY DEPENDENT ON MG2+ (BY SIMI-SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY: TO OTHER PPASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 DGDPLDILVITTNPPFPGCVIDTRVIGYLNMVDSGEEDAKLIGVPVEDP---RFDEVRSI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         , 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
23; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
28; Conser
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                                                                                                                                                   (PPASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PPASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRUCIFERAE
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larity 37.1%;
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                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                      CRENARCHAEOTA;
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33.3%;
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                       PARTIAL
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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                       SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 151; DB 1;
Pred. No. 8.03e-10;
18; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 154; DB 1;
Pred. No. 2.31e-10;
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                                                                      SULFOLOBALES
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                     AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 AA.
                                                                                                                                                                                                  UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 263;
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MEYER W., MOLL R., KATH T., SCHAFER G.;

ARCH. BIOCHEM. BIOPHYS. 319:149-156(1995).

-i- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)0 = 2

-i- COFACTOR: ABSOLUTE REQUIREMENT FOR MAGNESIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYDROLASE; MAGNESIUM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
101-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
101-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MITCHELL S.J., MINNICK M.F.;
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA E
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA E
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA E
-i- CATALYTIC ACTIVITY DYNAMICS REQUIRES THE PRESENCE
-i- COFACTOR: THIS ENZYME REQUIRES THE PRESENCE THE PRESEN
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   IPYR_SOLTU
Q43187;
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L; x81842; G886704; -.
SITE; PS00387; PPASE; 1.
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                                                                                                                                                                                                                                                                                                                                                              66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATION. MAGNESIUM CONFERS THE HIGHEST CATIONS PER SUBUNIT (BY SIMILARITY). SUBUNIT: HOMOHEXAMER (BY SIMILARITY). SUBCELLULAR LOCATION: CYTOPLASMIC. SIMILARITY: TO OTHER PPASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGDPLDVLVITNYQLXP-GSVIEVRPIĞILYMKDEEGEDAKIVAVPKDKTDPS-FSNIKD 119
                                                                 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKRLKPGYLEATVDWFRRYKVPD-GK 199
                                                                                                                                                                                                                                                                                                                                                       DSDPIDVLVCNTRPLIPGCVINVRPIGALIMEDDGGKDEKIIAVPTPKL-TQQYIGIHDY 124
                                                                                                                                                        KRLKPGYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWKAL
                                                                                                                                                                                                  TDLTENILKKIEHFFKHYK--DLEAGK-WAKIEGWRDKNFARELIQQAIERAKAI 176
                                                                                                                                                                                                                                                                                               L46591; G940255; -.
rE; PS00387; PPASE; 1.
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Similarity 33.7%;
29; Conservative
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Similarity 30.4%;
35; Conservative
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19381 'MW;
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20064 MW;
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Pred. No. 1.83e-09;
22; Mismatches 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 147; DB 1;
Pred. No. 4.16e-09
23; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                211 AA.
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(2)0 - 2 ORTHOPHOSPHATE.
ESENCE OF DIVALENT METAL
ACTIVITY. BINDS 4 DIVAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                          53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
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DIVALENT
                                                                                                                                                                                230
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RP OCC OR DET
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                                                                      STANDARD BEAUTION OF THE STANDARD BEAUTION OF 
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Best Local S
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Query Match
Best Local S
Matches 1
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01-NOV-1997 (REL. 3
01-NOV-1997 (REL. 3
SOLUBLE INORGANIC F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPA.
SOLANUM TUBEROSUM (POTATO).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
SOLANALES; SOLANACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DU JARDÍN P., ROJAS-BELTRAN J., GEBHARDT PHYSTOL. 109:853-860(1995).
PLANT PHYSTOL. 109:853-860(1995).
-!- COFACTOR: ACTIVITY DEPENDENT ON MG2+.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYDROLASE) (PPASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYDROLASE; MAGNESIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                         HYDROLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPYR_MYCPN
P75250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYCOPLASMA PNEUMONIAE. PROKARYOTA; TENERICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYDROLASE)
                                                                                                                                -:- SIMILARITY: TO OTHER PPASES. EMBL; AE000029; G1673987; -. PROSITE; PS00387; PPASE; 1.
                                                                                                                                                                                    STRAIN-ATCC 29342
MEDLINE; 97105885
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYCOPLASMATACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INORGANIC
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
CTRAIN-AICC 29342 / M129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 CGDNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDIN
                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                    HIMMELREICH R., HILBERT H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154
                                                                                                                                                                                                                                                                                                                                 IERRMANN R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95
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SIMILARITY: TO OTHER PPASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CEDNDPMDVLVLMQEPVLPGCFLRARAIGLMPMIDQGEKDDKIIAVCADDPEYRHYTDI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVKRLKPGYLEATVDWFRRYKVPDGK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --KOLPPHRLAEIRRFFEDYKKNENK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z36894; G534916; -.
NE; PS00387; PPASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 32; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96163189
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                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PPASE).
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larity 37:2%;
Conservative
                                                                          184
                                                                                                             MAGNESIUM.
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35, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
PYROPHOSPHATASE (EC 3.6.1.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35, CREATED)
35, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
35PHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 F
24261 MW;
                    5.9%;
28.6%;
                                                                          21369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLLICUTES; MYCOPLASMA;
                                                                            WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
16; M
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8F8FC92C CRC32;
  Score
Pred.
22; M
                                                                                                                                                                                                                                                                                                                                                          PLAGENS H.,
                                                                                               ВY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                D5F880FD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
  re 125; DB 1; I
d. No. 2.43e-05;
Mismatches 20;
                                                                                               SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147; DB 1;
No. 4.16e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   c.,
                                                                            CRC32;
                                                                                                                                                                                                                                                                                                                                                            PIRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                        (2)0:= 2 ORTHOPHOSPHATE:
ESENCE OF DIVALENT METAL
ACTIVITY. BINDS 4 DIVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BRASSEUR R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PYROPHOSPHATE PHOSPHO-
        20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                         Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYCOPLASMATALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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        Indels
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          Gaps
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18;

Conservative

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Search completed: Thu Sep 17 16:54:43 1998 Job time: 58 secs.
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                                                                                                                                                                                                                                                                         Query Match 5.7%;
Best Local Similarity 29.6%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCIENCE 269:496-512(1995).

SCIENCE 269:496-512(1995).

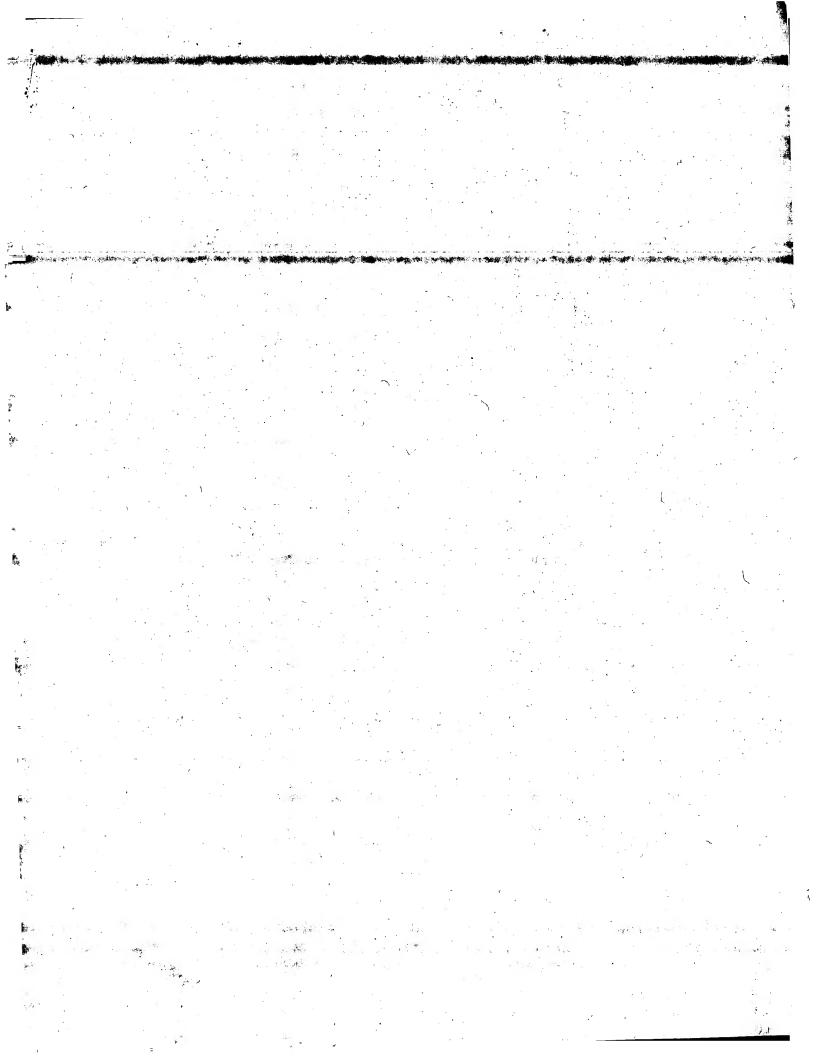
CATALTTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.

COFACTOR: THIS ENZYME REQUIRES THE PRESENCE OF DIVALENT METAL

CATION. MAGNESIUM CONFERS THE HIGHEST ACTIVITY. BINDS 4 DIVALENT

CATIONS PER SUBUNIT (BY SIMILARITY).

CATIONS PER SUBUNIT: HOMOHEXAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPYR_HAEIN P44529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.
KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.
MCKERNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
SCOTT J.D., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E.M., BRANDON R.C.,
FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
FRIED L.D., FRITCHMAN J.L., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-RD / KW20;
MEDLINE; 95350630.
                                                                                                                                                                                                                                                                                                                                                                                              HYDROLASE; MAGNESIUM. ACT_SITE 31 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAEMOPHILUS INFLUENZAE.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (REL.
01-NOV-1995 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            )1-NOV-1995 (REL.
01-NOV-1995 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 YKV 195
                                                                                      175 VKRLKPGYLEATVDW-FRRYKVPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWK 228
                                                                                                                              127 ---L-PANLIKQIEFHFNNYKALK-KPGST-KV-THWGDVEEAKEVIRESIKRWN 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               !- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROBABLE INORGANIC PYROPHOS HOSPHO-HYDROLASE) (PPASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                !- SIMILARITY: TO OTHER PPASES.
MBL; U32698; G1573079; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASTEURELLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 YKL 131
                                                                                                                                                                                116 DNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAAN-YNDIND 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
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                                                                                                                                                                                                             67 DGDELDVLLITRQPLATGVFLEAKVIGVMKFVDDGEVDDKIVCVPADDRDTGNAYNSLAD 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00387; PPASE; 1.
                                                                                                                                                                                                                                                                                                                                                                    31 31 I
176 AA; 19725 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32, CREATED)
32, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDATE)
C PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC.
                                                                                                                                                                                                                                                                         Score 122; DB 1;
Pred. No. 7.51e-05;
26; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
; CE8BDD6F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOUGHERTY B.A., MERRICK J.M.,
                                                                                                                                                                                                                                                                              46;
                                                                                                                                                                                                                                                                                                                    Length 176;
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                         9;
                                                                                                                                                                                                                                                                         Gaps
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\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\* (MT)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated Thu Sep 17 16:55:00 1998; MasPar time 18.79 Seconds 647.612 Million cell updates/sec

Description: Perfect Score: Sequence: >US-08-741-437-1 (1-289) from US08741437.pep 2134 1 MSGFSTEERAAPFSLEYRVF.....CESACTVPTDVDKWFHHQKN 289

Scoring table: PAM 150 Gap 11

Searched: 140555 segs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:sp\_fungi 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal 5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant 9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate

13:sp\_unclassified

Statistics: Mean 46.257; Variance 82.300; scale 0.562

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

18 102 4.	18 102 4.	L' LU4 4.	101			107 5		12 106 5.		108 5	117 5	ر.	5	6 135 6.	6	7	3 864 40.5			Result Query
356	8 181	8 91	9 358	9 181	0 377	•	_	0 356	1 482		-			3 176	7 215			1 285	4 292	Length
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000445	029766	Q95555	Q30593	Q954.09	019445	Q08680	Q30914	Q30444	Q41676	Q30223	034955	022537	Q49071	026363	023979	005724	P87118	013505	Q18680	ID
	TANTICEN	(STRAIN BM6) ALPHA-2 D	MHC CLASS I ANTIGEN MA	MHC CLASS I A ANTIGEN	MHC CLASS IB ANTIGEN.	RT1 CLASS I HISTOCOMPA	MHC CLASS I A (FRAGMEN	MHC CLASS I CAJA-G*04	LEGUMIN A PRECURSOR.	MHC CLASS I ATBE-G*03	INORGANIC PYROPHOSPHAT	INORGANIC PYROPHOSPHAT	INORGANIC PYROPHOSPHAT	INORGANIC PYROPHOSPHAT	SOLUBLE INORGANIC PYRO	PYROPHOSPHATASE (FRAGM	HYPOTHETICAL 32.9 KD P	INORGANIC PYROPHOSPHAT	HYPOTHETICAL PROTEIN C	Description
1.010.01	1 316-01	1.81e-01	9.43e-02	9.43e-02	3.49e-02	3.49e-02	3.49e-02	4.87e-02	1.78e-02	2.50e-02	1.12e-03	1.30e-04	4.35e-05	1.50e-06	6.87e-08	8.78e-10	1.72e-164	2.86e-197	6.23e-224	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	
99	99	99	98	99	98	99	98	99	99	99	99	101	101	101	101	100	100	100	101	100	101	101	103	103	
4.6	. 4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.8	4.8	
366	366	366	358	357	356	347	246	181	91	91	91	3063	365	363	363	354	354	344	294	181	166	166	1462	362	
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Q29864	Q31605	Q29991	Q30291	Q30917	Q30171	Q29505	Q29945	019505	019635	P79617	Q31189	Q99715	019756	Q29840	019642	Q95513	Q95514	P79602	Q30714	019354	Q95516	Q95518	034313	P79523	
CHAIN E	ALPHA CHAIN OF MHC CLA	HLA CLASS I HEAVY CHAI	1 PR	MHC CLASS I A (FRAGMEN	LYMPHOCYTE ANTIGEN.	GALACTOSIDE 2-L-FUCOSY	MHC CLASS I HLA-A CELL	HLA-CW6 (FRAGMENT).	MHC CLASS I ANTIGEN HL	MHC CLASS I HLA-C (FRA	MHC CLASS I H2-K-ALPHA	COLLAGEN TYPE XII ALPH	MHC CLASS I HLA-A.	MHC HLA-A*0301 BLANK G	MHC CLASS I ANTIGEN HL	HISTOCOMPATIBILITY ANT	HISTOCOMPATIBILITY ANT			MHC CLASS I A ANTIGEN		HISTOCOMPATIBILITY ANT	YFKN PROTEIN.	MHC CLASS I HISTOCOMPA	
4.74e-01	4.74e-01	4.74e-01	.49e	4.74e-01		4.74e-01		4.74e-01	4.74e-01	4.74e-01	4.74e-01	2.50e-01	2.50e-01		. 50			3.45e-01	· 2.50e-01	3.45e-01	.50e-	2.50e-01	.31e-	1.31e-01	

## ALIGNMENTS

Db 70 TKEPFSPIKQDEKKGVAREVHNIFPHKGYIWNYGALPQTWEDPNHVVPDTGAKGDNDPID 129	
Cy 4 FSTEERAAPFSLEYRVFLKNEKGQYISPFHDIPIXADKDVFHMYVEVPRWSNAKMEIA 61	
GPQG-I	
Query Match 52.4%; Score 1119; DB 3; Length 292; Best Local Similarity 53.2%; Pred. No. 6.23e-224; Matches 150; Conservative 65; Mismatches 60; Indels 7; Gaps 6;	
SEQUENCE 29	
DR EMBL; Z68882; E348322; -	
NATURE 368:32-38(1994).	
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;	
RA THIERRY-MIRG I THOMAS K VAHIDIN M VAHIGHAN K WATERSTON R	
PARSONS J., PERCY C., R	
RA LIGHTNING T. LICYD C. MCMIRRAY A. MORTIMORF R. CYCALLAGHAN M.	
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JO	
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,	
BONFIELD J., BURTON J., CONNELL M., COPSEY T., CO	
RP SEQUENCE FROM N.A.  RX MEDITURE 94150718	
[2]	
COLES L.;	
RP SEQUENCE FROM N.A.	
OC EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.	
C4/ELV.4.	
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION	
01-JAN-1998 (TREMBLREL, 05,	
1996 (TREMBLREL.	
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SUBMITTED (NOV-1997) TO EMB
EMBL; AJO01000; E1180018; -
HYDROLASE; PLASMID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998
01-JAN-1998
01-JAN-1998
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013505;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 VCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRLKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PICHIA PASTORIS (YEAST).
PLASMID PRS316-GAL1.
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)1-JAN-1998 (TREMBLREL. 05,
)1-JAN-1998 (TREMBLREL. 05,
)NORGANIC PYROPHOSPHATASE (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UKARYOTA;
                                                                                                                                                 P87118
P87118;
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BADCOCK
          SEQUENCE FROM N.A.
STRAIN-972H-;
                                                      EUKARYOTA; FUNGI;
                                                                                  SPAC3A12.02
                                                                                                 01-TUL-1997 (TREMBLREL. 04, CREATED)
01-TUL-1997 (TREMBLREL. 04, LAST SEQUENCE UF
01-TUL-1997 (TREMBLREL. 04, LAST ANNOTATION
HYPOTHETICAL 32.9 KD PROTEIN.
                                                                                                                                                                                                                                                                            179
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                                                                  SCHIZOSACCHAROMYCES POMBE
                                                                                                                                                                                                                        239
                                                                                                                                                                                                                                                                                                                                                                                                         59 EISKEEKLNPILQDTKKGKLREVRNCEPHHGYIHNYGAFPQTWEDPNVTHPETKAKGDND 118
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                                                                                                                                                                                                                    GISCMNTTLSESPFKCDPDAARAIVDALPPPCESACTVPTDVDKWF 284
                                                                                                                                                                                                                                                                            KPGYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWKALVTKKTNGK 238
                                                                                                                                                                                                                                                                                          MPGLLRATNEWERIYKIPDGKPENQFAFSGECKNKKYAEEVIQECREAWEKLIFGKTSPG 237
                                                                                                                                                                                                                                                                                                                                  PIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRL
                                                                                                                                                                                                                                                                                                                                                                                    EIATKDPLNPIKQDVKKGKLRYVANLFPYKGYIWNYGAIPQTWEDPGHNDKHTGCCGDND 118
                                                                                                                                                                                                                                             EIDLTNTTLOSTP-SFSPSATSAVPTA-SPA-APA-KIDQSIDKWF
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Similarity 52.48;
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 CHURCHER C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                  PRELIMINARY;
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                                                      ASCOMYCOTINA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PYROPHOSPHATE PHOSPHO-HYDROLASE) (EC
                                                         (FISSION YEAST).
OTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1005; DB 1;
Pred. No. 2.86e-197;
56; Mismatches 71;
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                                                                                                                                                                      PRT;
                                                                                                                             SEQUENCE UPDATE)
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DATA
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                                                                                                                                                                                                                                                       279
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Best Local Simil
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Best Local S
Matches 2
                                                                                                                                                                                                                                    SATOH T., ISHII K., KOYAMA M., SAKURAI N., K
IRIE M., SAMEJIMA T.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DAY
EMBL; AB003087; D1020624; -
NON_TER 164 164
SEQUENCE 164 AA; 18796 MW; BD71D735 CPC-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED (MAY-1997) TO E EMBL; Z95395; E316097; -- HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-972H-;
WOOD V:, BARR
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01-JUL-1997
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               01-JAN-1998
01-JAN-1998
01-JAN-1998
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                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                            PMK2PPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201
                                                023979
023979;
                                                                                                                                                                                                                                                                                                                                                       ROKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 EYRVF-LKNEKGQYISPFHDIPIYADKDVFHMVVEVPRWSNAKMEIATKDPLNPIKQDVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113
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                                                                                                      176 KRLKPGYLEATVDWFRRYKVPDGK
                                                                                                                                                                   56 DGDPLDILVITINPTFPGCVIDTRVIGYLNMYDSGEEDAKLIGVPVEDP---RFDEVRSI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IKQVKVLGALGLIDQGETDWKILAIDINDPRAKLLNDISDVQNLMPRLLPCTRDWFAIYK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGKLRYVANLEPYKGYIWNYGAIPQTWEDPGHNDKHTGCCGDNDPIDVCEIGSKVCARGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPDGKPENEFAFNAEFKDKDFAIDIIKSTHDHWKALVTKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRLKPGYLEATVDWFRRYK
                                                                                                                         EDLPQHKLKEIAHFFERYKDLQGK 136
                                                                                                                                                 DNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDV
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                                                                                                                                                                                             Similarity
28; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                 (TREMBLREL 04, TREMBLREL 04, TREMBLREL 04,
                 (TREMBLREL.
(TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                       FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                              Conservative
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                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.5%;
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                                                                                                                                                                                                                                                                                                                                                       ENDOSPORE-FORMING
                  0505
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; CREATED)
;, LAST SEQUENCE UPDATE)
5; LAST ANNOTATION UPDATE)
7 TANTASE (EC 3.6.1.1).
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                              Score 154; DB 9;
Pred. No. 8.78e-10;
18; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                          199
                                                                 PRT;
                                                                                                                                                                                                                                          BD71D735 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
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Best Local S
Matches 2
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Best Local
Q49071
Q49071;
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01-JAN-1998
01-JAN-1998
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VISSER K., HEIMOVAARA-DIJKSTRA S., KIJNE J.W.,
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL; AF009675; G2258074; -.
HYDROLASE.
                                                                                                                                                                                                                            SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL; AE000812; G2621313; -. SEQUENCE 176 AA; 20084 MW; 66900C6C CRC32;
                                                                                                                                                                                                                                                                                                                                                                            SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DU ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K., HARRISON D., HOANG L., KEACLE P., LUMM W., POTHIER B., QIU D. SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R., SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HORDEUM VULGARE VAR. DISTICHUM (TWO-ROWED BARLEY).
EUKARYOTAE; MITOCHONDRIAL EUKARYOTES; VIRIDIPLANTAE;
CHAROPHYTA/EMBRYOPHYTA GROUP; EMBRYOPHYTA; VASCULAR PLANTS;
SEED PLANTS: MAGNOLIOPHYTA; LILIOPSIDA; POALES; POACEAE; HO
                                                                                                                                                                                                                                                                     SMITH D.R.;
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REE J. BACTERIOL. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-DELTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARCHAEBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        026363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HORDEUM VULGARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METHANOBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHANOBACTERIUM THERMOAUTOTROPHICUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INORGANIC PYROPHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 CEDNDPMDVLVLMQEPVIPGSFLRARAIGLMPMIDQGEKDDKIIAVCADDPEYRHYSTSV 160
                                                                                                                       116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161
                                                                                              126
                                                                                                                                                                                                                                                                                                                                                                   IWANI N., CARUSO A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             )26363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 NDVKRL 178
                                                                   176 KRLKPGYLEATVDWFRRYKVPDGK
                                                                                                                                               66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLLPRL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGDNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYN-DI 172
                                                                                           -P-EHN-LKEIANFFETYKKLEGK 146
                                                                                                                      DNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDV 175
                                                                                                                                             DGDPMDILVLMDEPTFPGCIIESRPIGLLRMIDGGDQDDKILAVPVADPHFADVKDISDI 125
                                                                                                                                                                          Similarity 34.5%;
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 24; Conser
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B (TREMBLREL.
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              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EURYARCHAEOTA;
                                                                                                                                                                                    34.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24049 MW;
                                                                                                                                                                                                                                                                                                                                                                  BUSH D., SAFER H., PATWELL D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,0,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                    Score 135; DB 9;
Pred. No. 1.50e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 143; DB 8;
Pred. No. 6.87e-08;
                                                                   199
              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METHANOBACTERIALES
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                                                                                                                                                                          Mismatches
              136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UPDATE)
                                                                                                                                                                                                                                                                                                                                       REEVE J.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WANG M.;
BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 215;
                                                                                                                                                                                              Length 176
                                                                                                                                                                                                                                                                                                                                                     CHURCH G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Best Local
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Best Local 9
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O34955;

01-JAN-1998 (TREMBLREL. 0

01-JAN-1998 (TREMBLREL. 0

01-JAN-1998 (TREMBLREL. 0
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LEE M.C., KIM C.S., EUN M.Y.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL; AF022733; G2570501; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORYZA SATIVA (RICE).
EUKAKYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; MONOCOTYLEDONEAB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
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                                                PPA
                                                                       INORGANIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYPERALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROKARYOTA; TENERICUTES; MOLLICUTES; MYCOPLASMA; MYCOPLASMATALES;
                                                                                                                                                                                                                                                                                               174
                                                                                                                                                                                                                                                                                                                                                157
                                                                                                                                                                                                                                                                                                                                                                                              114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NORGANIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176
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OL. MICROBIOL. 16:955-967(1995)
MBL; Z33286; G530477; -...
DOL TER. 1.1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                            86
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                                                                                                                                                                                                                                                                                             DVKRLKPGYLEATVDWFRRYKVPDGKP-E-NEFAFNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                          CEDGDPMDVLVLMQEQVVPGCFLRARAIGLMPMIDQGEKDDKIIAVRADDLNTAT-SGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -P-KH-YRXXXXXFFLQYKALQNK
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                                                                                                                                                                                                                                                                                                                      RKSPFTA-FKRSAV-FFEDYKKNENKEVAVNEF-FPAE
                                                                                                                                                                                                                                                                                                                                                                                            CGDNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDIN 173
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                                                                       PYROPHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYROPHOSPHATASE (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 AA;
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27343(KID);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.9%; Score 126; DB 9; 31.0%; Pred. No. 4.35e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15815 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23610 MW;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
22; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 123; DB 8;
Pred. No. 1.30e-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                               LAST SEQUENCE UPDATE)
                                                                                                                                               CREATED)
                                                                                                                                                                                                PRT;
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LEGIONELLA PNEUMOPHILA PROKARYOTA; GRACILICUT

GRACILICUTES;

SCOTOBACTERIA; AEROBIC RODS AND COCCI;

EGIONELLACEAE

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RANGOCCOC GN
                                                                                                                                                                                                                                                                                                                                                                                                                                 δõ
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RRRR CC CC DT DT AC
                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFECT IMMUN. 0:0-0(1997).
EMBL; AF031464; G2642277; -
EMBL; AF030232; G2613038; -
SEQUENCE 178 AA; 20049 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-AA10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                              Q30223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
MHC CLASS I ATBE-G*03 (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                     125
                                                                                                                                                                                                                      NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
CADAVID L.F., SHUFFLEBOTHAM C.,
WATKINS D.I.;
                                                                                                                                                                                                                                                                                                               ATBE-G.
ATELES BELZEBUTH (LONG-HAIRED
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 DGDEVDVLVITEVPLISGAVISCRAVGMLKMTDESGVDAKILAVFTTKL-SKMYQSMQTY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                   176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                          SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ
EMBL; U59650; G1389913: -
                                                                                                                                                                                                                                                  ROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KWAIK
                                                                                                 Q41676;
                                                                                                                                                        141 VLNEDLRSWTAADLAAQITQR-KWEAANAAERMRA-YLEGTCYEWLRRY-LENGK 192 ::: | |::: |||:| |:::|| :::|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KWAIK Y:
SEQUENCE FROM N.A. TISSUE-COTYLEDON; NONG V., BECKER C.
                                            VICIA NARBONENSIS.
EUKARYOTA; PLANTAE;
                                                                         01-JAN-1998
                                                                                01-NOV-1996
                                                                                                                                             146 MIDEGETDWKVIAINVDDPDAANYNDINDVKRLKPGYLEAT-VDWFRRYKVPDGK
                                                               EGUMIN A PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    QDI-POHLLLSIEHFFKHYKDLEEGK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRLKPGYLEATVD-WFRRYK-VPDGK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
24; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMUN. 66:0-0(1998)
                                                                                                                                                                                   Similarity
15; Conser
                                                                                                                                                                                                                                                    .ps00290;
                                      FABALES; FABACEAE
                                                                                                                                                                                                                         363 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                    .18;
.larity 27.3%;
Conservative
                                                                        (TREMBLREL.
                                                                                (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                     IG_MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20049 MW;
                                                                                                                                                                                                                        40827
                                               EMBRYOBIONTA;
    MUENTZ
                                                                                                                                                                                                                                                                                                                                                               01, CREATED)
01, LAST SEQUENCE UPDATE)
05, LAST ANNOTATION UPDATE)
                                                                           92,00
                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
21; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                      Score
Pred.
16; M
                                                                                  CREATED)
                                                                            LAST
                                                                                                                                                                                                                                                                                                                           SPIDER MONKEY)
VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E3505B05 CRC32;
                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                            0E4A568E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117;
No. 1.
                                                                                                                                                                                                                                                                                          RUIZ F.J.,
                                                                                                                                                                                        Mismatches
                                                                           SEQUENCE UPDATE)
ANNOTATION UPDATE)
                                                                                                                                                                                               108; DB 5;
No. 2.50e-02;
                                                  MAGNOLIOPHYTA; MAGNOLIOPSIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 9;
1.12e-03;
1.3e 37;
                                                                                                                                                                                                                                                                                                                                                                                                      363
                                                                                                                 482
                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                           DATA BANKS
                                                                                                                 B
                                                                                                                                                                                                                                                                                             YEAGER M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 178;
                                                                                                                                                                                                           Length 363;
                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                  MAMMALIA;
                                                                                                                                                                                                                                                                                               HUGHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                               A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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SEARBECCCER
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Best Local
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PROSITE;
                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED (NOV-1994) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                              Q30444;
Q1-NOV-1996
Q1-NOV-1996
Q1-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                   030444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133
                                                                                                                                                                                                                                                                                                       CADAVID L.F.,
WATKINS D.I.;
SUBMITTED (JUN
                                                                                                                                                                                                                                                                                                                                                          CALLITHRIX JACCHUS (EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 RY-KVPDGKPENEFAFNAEFKD-K-DFAIDIIK 221
                                                                                                                                                                                                                                                                                                                                                                                     MHC CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193
                                                                                                                                                                                                                                                                                                                                                   EUTHERIA;
                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                             EMBL; U59640;
                                                                                                                01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASIC CHAIN DERIVED FROM A
                                                                                               MHC CLASS I A (FRAGMENT).
PAN TROGLODYTES (CHIMPANZEE).
                                                                                                                                                                                         147 IDEGETDWKVIAINVDDPDAANYNDINDVKRLKPGYLEAT-VDWFRRYKVPDGK 199
                                                                                                                                                                                                  142 LNEDLRSWTAPDVAAQITQR-KWEAANEAER-RRAYLEGTCVEWLRRY-LENGK
                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFIDE BOND SIMILARITY: TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT:
EMBL; U10
PROSITE;
MHC.
                MCADAM S.N., BOYSON J.E., BONTROP R.E., WATKINS D.I J. IMMUNOL. 154:6421-6429 J. IMMUNOL. 154:6670; ...
                                                   SEQUENCE FROM N.A. MEDLINE: 95279794.
                                                                               EUTHERIA;
                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEIIGVKYLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRLKPGYLEATVDW-FR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDIIAVPTGNVLWMYNDODTP--VIAISLTDTGSSN-NOLDQIPR-R-FYLAGNQEQEFL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RYQREQGGKQEQENDGNNIFSGFKRDFLEDALN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z46803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00305;
                                                                                                                                                                                                                              Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                    PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482
                                                                                                                                                                                                                                                                                               (JUN-1996) TO 540; G1389927;
                                                                                                                                                                                                                                                                                                                                                                                               (TREMBLREL.)
(TREMBLREL.)
                                                                              PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEXAMER;
                                                                                                                                                                                                                                                                     356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                        METAZOA; CHORDATA;
                                                                                                                                                                                                                               5.0%;
larity 27.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                         SHUFFLEBOTHAM C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11S_SEED_STORAGE; 1.
                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY)
OTHER 11S SEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54667 MW;
                                                                                                                                                                                                                                                                                                                                                              (COMMON MARMOSET).
CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TO EMBL/GENBANK/DDBJ DATA EACH SUBUNIT IS COMPOSED EACH SUBUNIT IS COMPOSED TROM A SINGLE PRECURSOL
                                                                                                                                                                                                                                                                       39894 MW;
            IG_MHC;
                                                                                                                                                                                                                                                                                                                                                                                         (FRAGMENT).
                            -6429(1995).
                                                                                                                                                                                                                                                                                                                                                                                                 01, CREATED)
01, LAST SEQUENCE UPDATE)
01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                          EMBL/GENBANK/DDBJ
                                                                                                                              01,
                                                                                                                     05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 109;
Pred. No. 1.
21; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
; 901C5103
                                              LIU
                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                  Score 106; DB 5;
Pred. No. 4.87e-02
15; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                            VERTEBRATA;
                                                                                                                                                                                                                                                                        ECFF4FAE
                                               ×
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                                                                                                                                                                                                                                                                                                                             RUIZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STORAGE
                                                GARBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRECURSOR
                                                                                                                                                                                                                                                                                                                              F.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          356 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC32;
                                                                                                                                                              357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78e-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEINS (GLOBULINS)
                                                                                                                                                                                                                                                                                                                                                                   TETRAPODA;
                                                                                                                                                                                                                                                                                                             DATA BANKS
                                                                                                                                                             B
                                                   н
                                                                                             TETRAPODA;
                                                                                                                                                                                                                                                                                                                               YEAGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BANKS.
OF AN
OR AND I
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                                                    HUGHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N ACIDIC
                                                                                                                                                                                                                                                                                                                                X
                                                                                                                                                                                                                                                                                                                                                                     MAMMALIA;
                                                                                                                                                                                                                                                                                                                                  HUGHES
                                                                                                MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C AND
BY A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFT
             Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.0%;
Best Local Similarity 27.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                               LT 15
019445
019445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q08680;
                        STRAIN=LEW;
LAMBRACHT D., DUEVEL
SUBMITTED (NOV-1997)
                                                                                                                                                                                RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                   01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WALTER L., HEINE L., GUENTHER E.;
IMMUNOGENETICS 39:351-354(1994).
EMBL; X70066; G56610; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=LEW/GUN; TISSUE=CONA STIMULATED LYMPHOCYTES;
MEDLINE; 94222444.
WALTER L., HEINE L., GUENTHER E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                 SEQUENCE FROM N.A.
                                                                                            MEDLINE: 95278971.
LAMBRACHT D., WONIGEIT K.;
LAMBRACHTICS 41:375-379(1995).
                                                                                                                                         STRAIN-LEW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 LNEDLRSWTAADMAAQITQR-KWEAAHAAERLRA-YLEGTCVEWLRRY-LENGK 192
::| | ::| |::|| ::|| ::||
147 IDEGETDWKVIAINVDDPDAANYNDINDVKRLKPGYLEAT-YDWFRRYKVPDGK 199
                                                                                                                                                                                                                                          HC CLASS IB
                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                   180 -YLQGTCVEWLRRY 192
                                                                                                                                                                                                                                                                                                                                                                                                                         123
                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
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                                                                                                                                                      EQUENCE FROM N.A.
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nes 15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASS I
                                                                                                                                                                                                                                                                                                                                                                    GYLEAT-VDWFRRY 193
                                                                                                                                                                                                                                                                                                                                                                                                                         CEIGSKVCA-RG-EIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRLKP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDVGSDGSLLRGYDQFAYDGRDYLALNEDLKT-WMA-ADTAAQMTRNKWDQAGEAERHKA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TRANSMEMBRANE.
1 21
1 21
22 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TREMBLREL 01, CREATED)
(TREMBLEEL 01, LAST SEQUENCE UPDATE)
(TREMBLEL 05, LAST ANNOTATION UPDATE)
HISTOCOMPATIBILITY ANTIGEN, LW2 ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.0%;
larity 27.8%;
Conservative
                                                                                                                                                                                                                                          ANTIGEN.
                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41053 MW;
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39890 MW;
                          o,
                                                                                                                                                                                                                                                      05,
                        WONIGEIT K.;
EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                   CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 107; DB 5; L
Pred. No. 3.49e-02;
15; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 107; DB 5; Length 367
Pred. No. 3.49e-02;
19; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
RT1 CLASS I HISTOCOMPATIBILITY ANTIGEN,
LW2 ALPHA CHAIN.
60475057 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                               VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24BF11F7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367
                                                                                                                                                                                                                                                                                                             377 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Search completed: Thu Sep 17 Job time: 124 secs.
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Best Local Similarity 27.0%;
Matches 20; Conservative
                                                                                                                                                                                                                STRAIN-LEW;
LAMBRACHT D.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF025308; G2570821; -
SEQUENCE 377 AA; 42200 MW; 335C92C1 CRC32;
                                                           180 -YLQGTCVEWLRRY 192
||::| |:|:||
181 GYLEAT-VDWFRRY 193
                                                                                                                                                     122 CDVGSDGSLLRGYDQFAYDGRDYLALNEDLKT-WMA-ADTAAQMTRNKWDQAGEAERHKA 179
                                                                                                                       123 CEIGSKVCA-RG-EIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRLKP 180
                16:57:04 1998
                                                                                                                                                                                  Score 107; DB 5;
Pred. No. 3.49e-02
19; Mismatches 2
                                                                                                                                                                                     29;
                                                                                                                                                                                                               Length 377
                                                                                                                                                                                     Indels
                                                                                                                                                                                   6,
                                                                                                                                                                                   Gaps
```

